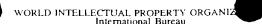
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(57) Abstract

The invention provides human phosphorylation effectors (PHSP) and polynucleotides which identify and encode PHSP. The invention also provides expression vectors, host cells, antibodies, agonists, and antagonists. The invention also provides methods for diagnosing, treating, or preventing disorders associated with expression of PHSP.

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PHOSPHORYLATION EFFECTORS

TECHNICAL FIELD

This invention relates to nucleic acid and amino acid sequences of phosphorylation effectors and to the use of these sequences in the diagnosis, treatment, and prevention of cell proliferative, immune, and neuronal disorders.

Kinases and phosphatases are critical components of intracellular signal transduction mechanisms. Kinases catalyze the transfer of high energy phosphate groups from adenosine triphosphate (ATP) to various target proteins. Phosphatases, in contrast, remove phosphate groups from proteins. Reversible protein phosphorylation is the main strategy for regulating protein activity in eukaryotic cells. In general, proteins are activated by phosphorylation in response to extracellular signals such as hormones, neurotransmitters, and growth and differentiation factors. 15 Protein dephosphorylation occurs when down-regulation of a signaling pathway is required. The coordinate activities of kinases and phosphatases regulate key cellular processes such as proliferation, differentiation, and cell cycle progression. Kinases comprise the largest known enzyme superfamily and are widely varied in their substrate specificities. Kinases may be categorized based on the specific amino acid residues that are phosphorylated in their substrates: protein tyrosine kinases (PTK) phosphorylate tyrosine residues, and protein serine/threonine kinases (STK) phosphorylate serine and/or threonine residues. Almost all kinases contain a conserved 250-300 amino acid catalytic domain. This domain can be further divided into 11 subdomains. N-terminal subdomains I-IV fold into a two-lobed structure which binds and orients the ATP donor molecule, and subdomain V spans the two lobes. C-terminal subdomains VIA-XI 25 bind the protein substrate and transfer the gamma phosphate from ATP to the hydroxyl group of a serine, threonine, or tyrosine residue. Each of the 11 subdomains contains specific catalytic residues or amino acid motifs characteristic of that subdomain. For example, subdomain I contains an 8-amino acid glycine-rich ATP binding consensus motif, subdomain II contains a critical lysine residue required for maximal catalytic activity, and subdomains VI and IX comprise 30 the highly conserved catalytic core. Kinases may also be categorized by additional amino acid sequences, generally between 5 and 100 residues, which either flank or occur within the kinase domain. These additional amino acid sequences regulate kinase activity and determine substrate specificity. (Reviewed in Hardie, G. and Hanks, S. (1995) The Protein Kinase Facts Books, Vol I:7-20 Academic Press, San Diego, CA.)

STKs include both protein kinase A (PKA) and calcium-dependent protein kinase C

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(PKC), both of which transduce signals from plasma membrane receptors. The activities of PKA and PKC are directly regulated by second messenger signaling molecules such as cyclic AMP and diacylglycerol, respectively. A novel kinase identified by genetic analysis in the fission yeast Schizosaccharomyces pombe is encoded by the cek1⁺ gene and is related to both PKA and PKC 5 (Samejima, I. and Yanagida, M. (1994) Mol. Cell. Biol. 14:6361-6371). cekI+ encodes an unusually large kinase of 1309 amino acids. The kinase domain spans residues 585 to 987, and 112 additional amino acids are present in this domain between subdomains VII and VIII. Overexpression of cek1 suppresses mutations in cut8, a gene required for chromosome segregation during mitosis. Therefore, cek1* may encode a unique member of the PKA/PKC protein family with a role in mitotic signaling and cell cycle progression.

PTKs may be classified as either transmembrane or nontransmembrane proteins. Transmembrane tyrosine kinases function as receptors for most growth factors. Binding of growth factor to the receptor activates the transfer of a phosphate group from ATP to selected tyrosine side chains of the receptor itself and other specific second messenger proteins. Growth factors 15 (GF) that associate with receptor PTKs include epidermal GF, platelet-derived GF, fibroblast GF, hepatocyte GF, insulin and insulin-like GFs, nerve GF, vascular endothelial GF, and macrophage colony stimulating factor. Nontransmembrane PTKs form signaling complexes with the cytosolic domains of plasma membrane receptors. Receptors that signal through nontransmembrane PTKs include cytokine, hormone, and antigen-specific lymphocytic receptors. Many PTKs were first identified as oncogene products in cancer cells in which PTK activation was no longer subject to normal cellular controls. In fact, about one third of the known oncogenes encode PTKs. Furthermore, cellular transformation (oncogenesis) is often accompanied by increased tyrosine phosphorylation activity (Charbonneau, H. and Tonks, N. K. (1992) Annu. Rev. Cell Biol. 8:463-93). Regulation of PTK activity may therefore be an important strategy in controlling some types of cancer.

Some kinases utilize carbohydrates as their substrates and are important for glucose metabolism. For example, glycolysis employs four distinct kinases to effect the conversion of glucose to pyruvate, a key metabolite in the production of ATP. One of these enzymes is phosphofructokinase (PFK) which catalyzes the transfer of phosphate from ATP to fructose 6-30 phosphate. PFK is an allosteric enzyme and a key regulator of glycolysis. In certain genetic muscle disorders, such as muscle phosphofructokinase deficiency type VII, phosphofructokinase activity is absent in muscle and deficient in red blood cells. As a result, afflicted individuals suffer from mild hemolytic anemia and muscle pain (Isselbacher, K.J. et al. (1994) Harrison's Principles of Internal Medicine, McGraw-Hill, New York, NY, p. 2102).

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Kinase-mediated phosphorylation is antagonized by the activity of phosphatases, which

remove phosphate groups by hydrolysis. Phosphatases are classified into one of three evolutionarily distinct families: the protein serine/threonine phosphatases (PPs), the protein tyrosine phosphatases, and the acid/alkaline phosphatases. PPs may be further categorized into four distinct groups: PP-I, PP-IIA, PP-IIB, and PP-IIC. (Cohen, P. (1989) Annu. Rev. Biochem. 58:453-508). PP-I, in particular, dephosphorylates many of the proteins phosphorylated by PKA and is therefore an important regulator of signal transduction pathways. Kinase-activated proteins which bind to and inhibit PP-I have been identified. These inhibitors potentiate the activity of kinases such as PKA by allowing protein substrates to remain in their phosphorylated, activated state. A novel inhibitor of PP-1 has been purified from porcine aorta (Eto, M. et al. (1995) J. 10 Biochem. 118:1104-1107; Eto, M. et al. (1997) FEBS Lett. 410:356-360). This inhibitor, called CPI17, is 147 amino acids in length and is activated by PKC. CPI17 expression is restricted to smooth muscle tissues such as aorta and bladder, suggesting that CPI17 functions in PKCmediated signal transduction pathways in these tissues, possibly through a calcium-dependent mechanism.

The discovery of new phosphorylation effectors and the polynucleotides encoding them satisfies a need in the art by providing new compositions which are useful in the diagnosis. prevention, and treatment of cell proliferative, immune, and neuronal disorders.

SUMMARY OF THE INVENTION

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The invention features substantially purified polypeptides, phosphorylation effectors, referred to collectively as "PHSP" and individually as "PHSP-1 to PHSP-31",. In one aspect, the invention provides a substantially purified polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-31, and fragments thereof.

The invention further provides a substantially purified variant having at least 90% amino acid identity to at least one of the amino acid sequences selected from the group consisting of SEO ID NO:1-31, and fragments thereof. The invention also provides an isolated and purified polynucleotide encoding the polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-31, and fragments thereof. The invention also includes an 30 isolated and purified polynucleotide variant having at least 80% polynucleotide sequence identity to the polynucleotide encoding the polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-31, and fragments thereof.

Additionally, the invention provides an isolated and purified polynucleotide which hybridizes under stringent conditions to the polynucleotide encoding the polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-31, and fragments

thereof. The invention also provides an isolated and purified polynucleotide having a sequence which is complementary to the polynucleotide encoding the polypeptide comprising the amino acid sequence selected from the group consisting of SEQ ID NO:1-31, and fragments thereof.

The invention also provides a method for detecting a polynucleotide in a sample 5 containing nucleic acids, the method comprising the steps of (a) hybridizing the complement of the polynucleotide sequence to at least one of the polynucleotides of the sample, thereby forming a hybridization complex; and (b) detecting the hybridization complex, wherein the presence of the hybridization complex correlates with the presence of a polynucleotide in the sample. In one aspect, the method further comprises amplifying the polynucleotide prior to hybridization.

The invention also provides an isolated and purified polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEO ID NO:32-62, and fragments thereof. The invention further provides an isolated and purified polynucleotide variant having at least 80% polynucleotide sequence identity to the polynucleotide sequence selected from the group consisting of SEQ ID NO:32-62, and fragments thereof. The invention also provides an 15 isolated and purified polynucleotide having a sequence which is complementary to the polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:32-62, and fragments thereof.

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The invention further provides an expression vector containing at least a fragment of the polynucleotide encoding the polypeptide comprising an amino acid sequence selected from the 20 group consisting of SEQ ID NO:1-31, and fragments thereof. In another aspect, the expression vector is contained within a host cell.

The invention also provides a method for producing a polypeptide, the method comprising the steps of: (a) culturing the host cell containing an expression vector containing at least a fragment of a polynucleotide under conditions suitable for the expression of the polypeptide; and (b) recovering the polypeptide from the host cell culture.

The invention also provides a pharmaceutical composition comprising a substantially purified polypeptide having the amino acid sequence selected from the group consisting of SEQ ID NO:1-31, and fragments thereof, in conjunction with a suitable pharmaceutical carrier.

The invention further includes a purified antibody which binds to a polypeptide selected 30 from the group consisting of SEQ ID NO:1-31, and fragments thereof. The invention also provides a purified agonist and a purified antagonist to the polypeptide.

The invention also provides a method for treating or preventing a disorder associated with decreased expression or activity of PHSP, the method comprising administering to a subject in need of such treatment an effective amount of a pharmaceutical composition comprising a 35 substantially purified polypeptide having the amino acid sequence selected from the group



consisting of SEQ ID NO:1-31, and fragments thereof, in conjunction with a suitable pharmaceutical carrier.

The invention also provides a method for treating or preventing a disorder associated with increased expression or activity of PHSP, the method comprising administering to a subject in need of such treatment an effective amount of an antagonist of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-31, and fragments thereof.

BRIEF DESCRIPTION OF THE TABLES

Table 1 shows nucleotide and polypeptide sequence identification numbers (SEQ ID NO), clone identification numbers (clone ID), cDNA libraries, and cDNA fragments used to assemble full-length sequences encoding PHSP.

Table 2 shows features of each polypeptide sequence, including potential motifs, homologous sequences, and methods and algorithms used for identification of PHSP.

Table 3 shows the tissue-specific expression patterns of each nucleic acid sequence as

determined by northern analysis, diseases, disorders, or conditions associated with these tissues,
and the vector into which each cDNA was cloned.

Table 4 describes the tissues used to construct the cDNA libraries from which cDNA clones encoding PHSP were isolated.

Table 5 shows the tools, programs, and algorithms used to analyze PHSP, along with applicable descriptions, references, and threshold parameters.

DESCRIPTION OF THE INVENTION

Before the present proteins, nucleotide sequences, and methods are described, it is understood that this invention is not limited to the particular machines, materials and methods described, as these may vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to limit the scope of the present invention which will be limited only by the appended claims.

It must be noted that as used herein and in the appended claims, the singular forms "a,"
"an," and "the" include plural reference unless the context clearly dictates otherwise. Thus, for
example, a reference to "a host cell" includes a plurality of such host cells, and a reference to "an
antibody" is a reference to one or more antibodies and equivalents thereof known to those skilled
in the art, and so forth.

Unless defined otherwise, all technical and scientific terms used herein have the same meanings as commonly understood by one of ordinary skill in the art to which this invention belongs. Although any machines, materials, and methods similar or equivalent to those described

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herein can be used to practice or test the present invention, the preferred machines, materials and methods are now described. All publications mentioned herein are cited for the purpose of describing and disclosing the cell lines, protocols, reagents and vectors which are reported in the publications and which might be used in connection with the invention. Nothing herein is to be construed as an admission that the invention is not entitled to antedate such disclosure by virtue of prior invention.

DEFINITIONS

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"PHSP" refers to the amino acid sequences of substantially purified PHSP obtained from any species, particularly a mammalian species, including bovine, ovine, porcine, murine, equine, 10 and preferably the human species, from any source, whether natural, synthetic, semi-synthetic, or recombinant.

The term "agonist" refers to a molecule which, when bound to PHSP, increases or prolongs the duration of the effect of PHSP. Agonists may include proteins, nucleic acids, carbohydrates, or any other molecules which bind to and modulate the effect of PHSP.

An "allelic variant" is an alternative form of the gene encoding PHSP. Allelic variants may result from at least one mutation in the nucleic acid sequence and may result in altered mRNAs or in polypeptides whose structure or function may or may not be altered. Any given natural or recombinant gene may have none, one, or many allelic forms. Common mutational changes which give rise to allelic variants are generally ascribed to natural deletions, additions, or 20 substitutions of nucleotides. Each of these types of changes may occur alone, or in combination with the others, one or more times in a given sequence.

"Altered" nucleic acid sequences encoding PHSP include those sequences with deletions, insertions, or substitutions of different nucleotides, resulting in a polynucleotide the same as PHSP or a polypeptide with at least one functional characteristic of PHSP. Included within this 25 definition are polymorphisms which may or may not be readily detectable using a particular oligonucleotide probe of the polynucleotide encoding PHSP, and improper or unexpected hybridization to allelic variants, with a locus other than the normal chromosomal locus for the polynucleotide sequence encoding PHSP. The encoded protein may also be "altered," and may contain deletions, insertions, or substitutions of amino acid residues which produce a silent change 30 and result in a functionally equivalent PHSP. Deliberate amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues, as long as the biological or immunological activity of PHSP is retained. For example, negatively charged amino acids may include aspartic acid and glutamic acid, positively charged amino acids may include lysine and arginine, and amino acids with 35 uncharged polar head groups having similar hydrophilicity values may include leucine, isoleucine,

and valine; glycine and alanine; asparagine and glutamine; serine and threonine; and phenylalanine and tyrosine.

The terms "amino acid" or "amino acid sequence" refer to an oligopeptide, peptide, polypeptide, or protein sequence, or a fragment of any of these, and to naturally occurring or synthetic molecules. In this context, "fragments," "immunogenic fragments," or "antigenic fragments" refer to fragments of PHSP which are preferably at least 5 to about 15 amino acids in length, most preferably at least 14 amino acids, and which retain some biological activity or immunological activity of PHSP. Where "amino acid sequence" is recited to refer to an amino acid sequence of a naturally occurring protein molecule, "amino acid sequence" and like terms are not meant to limit the amino acid sequence to the complete native amino acid sequence associated with the recited protein molecule.

"Amplification" relates to the production of additional copies of a nucleic acid sequence.

Amplification is generally carried out using polymerase chain reaction (PCR) technologies well known in the art.

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The term "antagonist" refers to a molecule which, when bound to PHSP, decreases the amount or the duration of the effect of the biological or immunological activity of PHSP.

Antagonists may include proteins, nucleic acids, carbohydrates, antibodies, or any other molecules which decrease the effect of PHSP.

The term "antibody" refers to intact molecules as well as to fragments thereof, such as

Fab, F(ab')₂, and Fv fragments, which are capable of binding the epitopic determinant. Antibodies that bind PHSP polypeptides can be prepared using intact polypeptides or using fragments containing small peptides of interest as the immunizing antigen. The polypeptide or oligopeptide used to immunize an animal (e.g., a mouse, a rat, or a rabbit) can be derived from the translation of RNA, or synthesized chemically, and can be conjugated to a carrier protein if desired. Commonly used carriers that are chemically coupled to peptides include bovine serum albumin, thyroglobulin, and keyhole limpet hemocyanin (KLH). The coupled peptide is then used to immunize the animal.

The term "antigenic determinant" refers to that fragment of a molecule (i.e., an epitope) that makes contact with a particular antibody. When a protein or a fragment of a protein is used to immunize a host animal, numerous regions of the protein may induce the production of antibodies which bind specifically to antigenic determinants (given regions or three-dimensional structures on the protein). An antigenic determinant may compete with the intact antigen (i.e., the immunogen used to elicit the immune response) for binding to an antibody.

The term "antisense" refers to any composition containing a nucleic acid sequence which is complementary to the "sense" strand of a specific nucleic acid sequence. Antisense molecules

may be produced by any method including synthesis or transcription. Once introduced into a cell,

the complementary nucleotides combine with natural sequences produced by the cell to form duplexes and to block either transcription or translation. The designation "negative" can refer to the antisense strand, and the designation "positive" can refer to the sense strand.

The term "biologically active," refers to a protein having structural, regulatory, or biochemical functions of a naturally occurring molecule. Likewise, "immunologically active" refers to the capability of the natural, recombinant, or synthetic PHSP, or of any oligopeptide thereof, to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

The terms "complementary" or "complementarity" refer to the natural binding of
polynucleotides by base pairing. For example, the sequence "5' A-G-T 3" bonds to the
complementary sequence "3' T-C-A 5'." Complementarity between two single-stranded molecules
may be "partial," such that only some of the nucleic acids bind, or it may be "complete," such that
total complementarity exists between the single stranded molecules. The degree of
complementarity between nucleic acid strands has significant effects on the efficiency and strength
of the hybridization between the nucleic acid strands. This is of particular importance in
amplification reactions, which depend upon binding between nucleic acids strands, and in the
design and use of peptide nucleic acid (PNA) molecules.

A "composition comprising a given polynucleotide sequence" or a "composition comprising a given amino acid sequence" refer broadly to any composition containing the given polynucleotide or amino acid sequence. The composition may comprise a dry formulation or an aqueous solution. Compositions comprising polynucleotide sequences encoding PHSP or fragments of PHSP may be employed as hybridization probes. The probes may be stored in freezedried form and may be associated with a stabilizing agent such as a carbohydrate. In hybridizations, the probe may be deployed in an aqueous solution containing salts (e.g., NaCl), detergents (e.g., sodium dodecyl sulfate; SDS), and other components (e.g., Denhardt's solution, dry milk, salmon sperm DNA, etc.).

"Consensus sequence" refers to a nucleic acid sequence which has been resequenced to resolve uncalled bases, extended using the XL-PCR kit (Perkin-Elmer, Norwalk CT) in the 5' and/or the 3' direction, and resequenced, or which has been assembled from the overlapping sequences of more than one Incyte Clone using a computer program for fragment assembly, such as the GELVIEW fragment assembly system (GCG, Madison WI). Some sequences have been both extended and assembled to produce the consensus sequence.

The term "correlates with expression of a polynucleotide" indicates that the detection of the presence of nucleic acids, the same or related to a nucleic acid sequence encoding PHSP, by northern analysis is indicative of the presence of nucleic acids encoding PHSP in a sample, and

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thereby correlates with expression of the transcript from the polynucleotide encoding PHSP.

A "deletion" refers to a change in the amino acid or nucleotide sequence that results in the absence of one or more amino acid residues or nucleotides.

The term "derivative" refers to the chemical modification of a polypeptide sequence, or a

5 polynucleotide sequence. Chemical modifications of a polynucleotide sequence can include, for
example, replacement of hydrogen by an alkyl, acyl, or amino group. A derivative polynucleotide
encodes a polypeptide which retains at least one biological or immunological function of the
natural molecule. A derivative polypeptide is one modified by glycosylation, pegylation, or any
similar process that retains at least one biological or immunological function of the polypeptide

from which it was derived.

The term "similarity" refers to a degree of complementarity. There may be partial similarity or complete similarity. The word "identity" may substitute for the word "similarity." A partially complementary sequence that at least partially inhibits an identical sequence from hybridizing to a target nucleic acid is referred to as "substantially similar." The inhibition of hybridization of the completely complementary sequence to the target sequence may be examined using a hybridization assay (Southern or northern blot, solution hybridization, and the like) under conditions of reduced stringency. A substantially similar sequence or hybridization probe will compete for and inhibit the binding of a completely similar (identical) sequence to the target sequence under conditions of reduced stringency. This is not to say that conditions of reduced stringency are such that non-specific binding is permitted, as reduced stringency conditions require that the binding of two sequences to one another be a specific (i.e., a selective) interaction. The absence of non-specific binding may be tested by the use of a second target sequence which lacks even a partial degree of complementarity (e.g., less than about 30% similarity or identity). In the absence of non-specific binding, the substantially similar sequence or probe will not hybridize to the second non-complementary target sequence.

The phrases "percent identity" and "% identity" refer to the percentage of sequence similarity found in a comparison of two or more amino acid or nucleic acid sequences. Percent identity can be determined electronically, e.g., by using the MEGALIGN program (DNASTAR, Madison WI) which creates alignments between two or more sequences according to methods selected by the user, e.g., the clustal method. (See, e.g., Higgins, D.G. and P.M. Sharp (1988) Gene 73:237-244.) The clustal algorithm groups sequences into clusters by examining the distances between all pairs. The clusters are aligned pairwise and then in groups. The percentage similarity between two amino acid sequences, e.g., sequence A and sequence B, is calculated by dividing the length of sequence A, minus the number of gap residues in sequence A, minus the number of gap residues in sequence A

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and sequence B, times one hundred. Gaps of low or of no similarity between the two amino acid sequences are not included in determining percentage similarity. Percent identity between nucleic acid sequences can also be counted or calculated by other methods known in the art, e.g., the Jotun Hein method. (See, e.g., Hein, J. (1990) Methods Enzymol. 183:626-645.) Identity between sequences can also be determined by other methods known in the art, e.g., by varying hybridization conditions.

"Human artificial chromosomes" (HACs) are linear microchromosomes which may contain DNA sequences of about 6 kb to 10 Mb in size, and which contain all of the elements required for stable mitotic chromosome segregation and maintenance.

The term "humanized antibody" refers to antibody molecules in which the amino acid sequence in the non-antigen binding regions has been altered so that the antibody more closely resembles a human antibody, and still retains its original binding ability.

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"Hybridization" refers to any process by which a strand of nucleic acid binds with a complementary strand through base pairing.

The term "hybridization complex" refers to a complex formed between two nucleic acid sequences by virtue of the formation of hydrogen bonds between complementary bases. A hybridization complex may be formed in solution (e.g., C_0 t or R_0 t analysis) or formed between one nucleic acid sequence present in solution and another nucleic acid sequence immobilized on a solid support (e.g., paper, membranes, filters, chips, pins or glass slides, or any other appropriate substrate to which cells or their nucleic acids have been fixed).

The words "insertion" or "addition" refer to changes in an amino acid or nucleotide sequence resulting in the addition of one or more amino acid residues or nucleotides, respectively, to the sequence found in the naturally occurring molecule.

"Immune response" can refer to conditions associated with inflammation, trauma, immune disorders, or infectious or genetic disease, etc. These conditions can be characterized by expression of various factors, e.g., cytokines, chemokines, and other signaling molecules, which may affect cellular and systemic defense systems.

The term "microarray" refers to an arrangement of distinct polynucleotides on a substrate.

The terms "element" or "array element" in a microarray context, refer to hybridizable polynucleotides arranged on the surface of a substrate.

The term "modulate" refers to a change in the activity of PHSP. For example, modulation may cause an increase or a decrease in protein activity, binding characteristics, or any other biological, functional, or immunological properties of PHSP.

The phrases "nucleic acid" or "nucleic acid sequence," as used herein, refer to a nucleotide, oligonucleotide, polynucleotide, or any fragment thereof. These phrases also refer to

DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA), or to any DNA-like or RNA-like material. In this context, "fragments" refers to those nucleic acid sequences which, comprise a region of unique polynucleotide sequence that specifically identifies SEQ ID NO:32-62, for example, as distinct from any other sequence in the same genome. For example, a fragment of SEQ ID NO:32-62 is useful in hybridization and amplification technologies and in analogous methods that distinguish SEQ ID NO:32-62 from related polynucleotide sequences. A fragment of SEQ ID NO:32-62 is at least about 15-20 nucleotides in length. The precise length of the fragment of SEQ ID NO:32-62 and the region of SEQ ID NO:32-62 to which the fragment corresponds are routinely determinable by one of ordinary skill in the art based on the intended purpose for the fragment. In some cases, a fragment, when translated, would produce polypeptides retaining some functional characteristic, e.g., antigenicity, or structural domain characteristic, e.g., ATP-binding site, of the full-length polypeptide

The terms "operably associated" or "operably linked" refer to functionally related nucleic acid sequences. A promoter is operably associated or operably linked with a coding sequence if the promoter controls the translation of the encoded polypeptide. While operably associated or operably linked nucleic acid sequences can be contiguous and in the same reading frame, certain genetic elements, e.g., repressor genes, are not contiguously linked to the sequence encoding the polypeptide but still bind to operator sequences that control expression of the polypeptide.

The term "oligonucleotide" refers to a nucleic acid sequence of at least about 6 nucleotides to 60 nucleotides, preferably about 15 to 30 nucleotides, and most preferably about 20 to 25 nucleotides, which can be used in PCR amplification or in a hybridization assay or microarray. "Oligonucleotide" is substantially equivalent to the terms "amplimer," "primer," "oligomer," and "probe," as these terms are commonly defined in the art.

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"Peptide nucleic acid" (PNA) refers to an antisense molecule or anti-gene agent which comprises an oligonucleotide of at least about 5 nucleotides in length linked to a peptide backbone of amino acid residues ending in lysine. The terminal lysine confers solubility to the composition. PNAs preferentially bind complementary single stranded DNA or RNA and stop transcript elongation, and may be pegylated to extend their lifespan in the cell.

The term "sample" is used in its broadest sense. A sample suspected of containing nucleic acids encoding PHSP, or fragments thereof, or PHSP itself, may comprise a bodily fluid; an extract from a cell, chromosome, organelle, or membrane isolated from a cell; a cell; genomic DNA, RNA, or cDNA, in solution or bound to a substrate; a tissue; a tissue print; etc.

The terms "specific binding" or "specifically binding" refer to that interaction between a protein or peptide and an agonist, an antibody, or an antagonist. The interaction is dependent upon

the presence of a particular structure of the protein, e.g., the antigenic determinant or epitope, recognized by the binding molecule. For example, if an antibody is specific for epitope "A," the presence of a polypeptide containing the epitope A, or the presence of free unlabeled A, in a reaction containing free labeled A and the antibody will reduce the amount of labeled A that binds to the antibody.

The term "stringent conditions" refers to conditions which permit hybridization between polynucleotides and the claimed polynucleotides. Stringent conditions can be defined by salt concentration, the concentration of organic solvent, e.g., formamide, temperature, and other conditions well known in the art. In particular, stringency can be increased by reducing the concentration of salt, increasing the concentration of formamide, or raising the hybridization temperature.

The term "substantially purified" refers to nucleic acid or amino acid sequences that are removed from their natural environment and are isolated or separated, and are at least about 60% free, preferably about 75% free, and most preferably about 90% free from other components with which they are naturally associated.

A "substitution" refers to the replacement of one or more amino acids or nucleotides by different amino acids or nucleotides, respectively.

"Substrate" refers to any suitable rigid or semi-rigid support including membranes, filters, chips, slides, wafers, fibers, magnetic or nonmagnetic beads, gels, tubing, plates, polymers, microparticles and capillaries. The substrate can have a variety of surface forms, such as wells, trenches, pins, channels and pores, to which polynucleotides or polypeptides are bound.

"Transformation" describes a process by which exogenous DNA enters and changes a recipient cell. Transformation may occur under natural or artificial conditions according to various methods well known in the art, and may rely on any known method for the insertion of foreign nucleic acid sequences into a prokaryotic or eukaryotic host cell. The method for transformation is selected based on the type of host cell being transformed and may include, but is not limited to, viral infection, electroporation, heat shock, lipofection, and particle bombardment. The term "transformed" cells includes stably transformed cells in which the inserted DNA is capable of replication either as an autonomously replicating plasmid or as part of the host chromosome, as well as transiently transformed cells which express the inserted DNA or RNA for limited periods of time.

A "variant" of PHSP polypeptides refers to an amino acid sequence that is altered by one or more amino acid residues. The variant may have "conservative" changes, wherein a substituted amino acid has similar structural or chemical properties (e.g., replacement of leucine with isoleucine). More rarely, a variant may have "nonconservative" changes (e.g., replacement of

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glycine with tryptophan). Analogous minor variations may also include amino acid deletions or insertions, or both. Guidance in determining which amino acid residues may be substituted, inserted, or deleted without abolishing biological or immunological activity may be found using computer programs well known in the art, for example, LASERGENE software (DNASTAR).

The term "variant," when used in the context of a polynucleotide sequence, may encompass a polynucleotide sequence related to PHSP. This definition may also include, for example, "allelic" (as defined above), "splice," "species," or "polymorphic" variants. A splice variant may have significant identity to a reference molecule, but will generally have a greater or lesser number of polynucleotides due to alternate splicing of exons during mRNA processing. The 10 corresponding polypeptide may possess additional functional domains or an absence of domains. Species variants are polynucleotide sequences that vary from one species to another. The resulting polypeptides generally will have significant amino acid identity relative to each other. A polymorphic variant is a variation in the polynucleotide sequence of a particular gene between individuals of a given species. Polymorphic variants also may encompass "single nucleotide 15 polymorphisms" (SNPs) in which the polynucleotide sequence varies by one base. The presence of SNPs may be indicative of, for example, a certain population, a disease state, or a propensity for a disease state.

THE INVENTION

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The invention is based on the discovery of new human phosphorylation effectors (PHSP), 20 the polynucleotides encoding PHSP, and the use of these compositions for the diagnosis, treatment, or prevention of cell proliferative, immune, and neuronal disorders.

Table 1 lists the Incyte clones used to assemble full length nucleotide sequences encoding PHSP. Columns 1 and 2 show the sequence identification numbers (SEQ ID NOs) of the polypeptide and nucleotide sequences, respectively. Column 3 shows the clone IDs of the Incyte 25 clones in which nucleic acids encoding each PHSP were identified, and column 4 shows the cDNA libraries from which these clones were isolated. Column 5 shows Incyte clones and their corresponding cDNA libraries. Clones for which cDNA libraries are not indicated were derived from pooled cDNA libraries. The clones in column 5 were used to assemble the consensus nucleotide sequence of each PHSP and are useful as fragments in hybridization technologies.

The columns of Table 2 show various properties of each of the polypeptides of the invention: column 1 references the SEQ ID NO and column 2 shows the number of amino acid residues in each polypeptide. Columns 3 and 4 show potential phosphorylation sites and potential glycosylation sites, respectively. Column 5 shows the amino acid residues comprising signature sequences and motifs. Column 6 shows homologous sequences as identified by BLAST analysis, 35 while column 7 shows analytical methods used to identify each polypeptide through sequence

homology and protein motifs.

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The columns of Table 3 show the tissue-specificity and diseases, disorders, or conditions associated with nucleotide sequences encoding PHSP. The first column of Table 3 lists the SEQ ID NOs. Column 2 lists tissue categories which express PHSP as a fraction of total tissue categories expressing PHSP. Column 3 lists diseases, disorders, or conditions associated with those tissues expressing PHSP. Column 4 lists the vectors used to subclone the cDNA library.

The columns of Table 4 show descriptions of the tissues used to construct the cDNA libraries from which cDNA clones encoding PHSP were isolated. Column 1 references the SEQ ID NO, column 2 shows the cDNA libraries from which these clones were isolated, and column 3 shows the tissue origins and other descriptive information relevant to the cDNA libraries in column 2.

The following fragments of the nucleotide sequences encoding PHSP are useful, for example, in hybridization or amplification technologies to identify SEQ ID NO:32-62 and to distinguish between SEQ ID NO:32-62 and related polynucleotide sequences. The useful 15 fragments include, the fragment of SEQ ID NO:32 from about nucleotide 81 to about nucleotide 110; the fragment of SEQ ID NO:33 from about nucleotide 323 to about nucleotide 352; the fragment of SEQ ID NO:34 from about nucleotide 83 to about nucleotide 112; the fragment of SEQ ID NO:35 from about nucleotide 524 to about nucleotide 553; the fragment of SEO ID NO:36 from about nucleotide 275 to about nucleotide 346; the fragment of SEQ ID NO:37 from about nucleotide 1328 to about nucleotide 1396; the fragment of SEQ ID NO:38 from about nucleotide 245 to about nucleotide 304; the fragment of SEQ ID NO:39 from about nucleotide 1253 to about nucleotide 1312; the fragment of SEQ ID NO:41 from about nucleotide 117 to about nucleotide 170; the fragments of SEQ ID NO:42 from about nucleotide 109 to about nucleotide 153, and from about nucleotide 325 to about nucleotide 369; the fragments of SEQ ID NO:43 from 25 about nucleotide 380 to about nucleotide 424, and from about nucleotide 1190 to about nucleotide 1234; the fragment of SEQ ID NO:44 from about nucleotide 1 to about nucleotide 46; the fragment of SEQ ID NO:45 from about nucleotide 533 to about nucleotide 577; the fragments of SEQ ID NO:46 from about nucleotide 109 to about nucleotide 153, and from about nucleotide 379 to about nucleotide 423; the fragment of SEQ ID NO:47 from about nucleotide 1730 to about 30 nucleotide 1774; the fragment of SEQ ID NO:48 from about nucleotide 433 to about nucleotide 477; the fragment of SEQ ID NO:49 from about nucleotide 1117 to about nucleotide 1155; the fragment of SEQ ID NO:50 from about nucleotide 166 to about nucleotide 213; the fragment of SEQ ID NO:51 from about nucleotide 60 to about nucleotide 95; the fragment of SEQ ID NO:52 from about nucleotide 326 to about nucleotide 370; the fragment of SEQ ID NO:53 from about 35 nucleotide 25 to about nucleotide 66; the fragment of SEQ ID NO:54 from about nucleotide 55 to

about nucleotide 102; the fragment of SEQ ID NO:55 from about nucleotide 138 to about nucleotide 167; the fragment of SEQ ID NO:56 from about nucleotide 29 to about nucleotide 58; the fragment of SEQ ID NO:57 from about nucleotide 455 to about nucleotide 484; the fragment of SEQ ID NO:58 from about nucleotide 226 to about nucleotide 255; the fragment of SEQ ID NO:59 from about nucleotide 557 to about nucleotide 598; the fragment of SEQ ID NO:60 from about nucleotide 284 to about nucleotide 325; the fragment of SEQ ID NO:61 from about nucleotide 1043 to about nucleotide 1090; and the fragment of SEQ ID NO:62 from about nucleotide 84 to about nucleotide 132. The polypeptides encoded by the fragments of SEQ ID NO:32-62 are useful, for example, as immunogenic peptides.

The invention also encompasses PHSP variants. A preferred PHSP variant is one which has at least about 80%, more preferably at least about 90%, and most preferably at least about 95% amino acid sequence identity to the PHSP amino acid sequence, and which contains at least one functional or structural characteristic of PHSP.

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The invention also encompasses polynucleotides which encode PHSP. In a particular embodiment, the invention encompasses a polynucleotide sequence comprising a sequence selected from the group consisting of SEQ ID NO:32-62, which encodes PHSP.

The invention also encompasses a variant of a polynucleotide sequence encoding PHSP. In particular, such a variant polynucleotide sequence will have at least about 80%, more preferably at least about 85%, and most preferably at least about 95% polynucleotide sequence identity to the polynucleotide sequence encoding PHSP. A particular aspect of the invention encompasses a variant of a polynucleotide sequence comprising a sequence selected from the group consisting of SEQ ID NO:32-62 which has at least about 80%, more preferably at least about 85%, and most preferably at least about 95% polynucleotide sequence identity to a nucleic acid sequence selected from the group consisting of SEQ ID NO:32-62. Any one of the polynucleotide variants described above can encode an amino acid sequence which contains at least one functional or structural characteristic of PHSP.

It will be appreciated by those skilled in the art that as a result of the degeneracy of the genetic code, a multitude of polynucleotide sequences encoding PHSP, some bearing minimal similarity to the polynucleotide sequences of any known and naturally occurring gene, may be produced. Thus, the invention contemplates each and every possible variation of polynucleotide sequence that could be made by selecting combinations based on possible codon choices. These combinations are made in accordance with the standard triplet genetic code as applied to the polynucleotide sequence of naturally occurring PHSP, and all such variations are to be considered as being specifically disclosed.

Although nucleotide sequences which encode PHSP and its variants are preferably capable of hybridizing to the nucleotide sequence of the naturally occurring PHSP under appropriately selected conditions of stringency, it may be advantageous to produce nucleotide sequences encoding

PHSP or its derivatives possessing a substantially different codon usage, e.g., inclusion of non-naturally occurring codons. Codons may be selected to increase the rate at which expression of the peptide occurs in a particular prokaryotic or eukaryotic host in accordance with the frequency with which particular codons are utilized by the host. Other reasons for substantially altering the nucleotide sequence encoding PHSP and its derivatives without altering the encoded amino acid sequences include the production of RNA transcripts having more desirable properties, such as a greater half-life, than transcripts produced from the naturally occurring sequence.

The invention also encompasses production of DNA sequences which encode PHSP and PHSP derivatives, or fragments thereof, entirely by synthetic chemistry. After production, the synthetic sequence may be inserted into any of the many available expression vectors and cell systems using reagents well known in the art. Moreover, synthetic chemistry may be used to introduce mutations into a sequence encoding PHSP or any fragment thereof.

Also encompassed by the invention are polynucleotide sequences that are capable of hybridizing to the claimed polynucleotide sequences, and, in particular, to those shown in SEO ID 15 NO:32-62 and fragments thereof under various conditions of stringency. (See, e.g., Wahl, G.M. and S.L. Berger (1987) Methods Enzymol. 152:399-407; Kimmel, A.R. (1987) Methods Enzymol. 152:507-511.) For example, stringent salt concentration will ordinarily be less than about 750 mM NaCl and 75 mM trisodium citrate, preferably less than about 500 mM NaCl and 50 mM trisodium citrate, and most preferably less than about 250 mM NaCl and 25 mM trisodium citrate. Low stringency hybridization can be obtained in the absence of organic solvent, e.g., formamide, while high stringency hybridization can be obtained in the presence of at least about 35% formamide, and most preferably at least about 50% formamide. Stringent temperature conditions will ordinarily include temperatures of at least about 30°C, more preferably of at least about 37°C, and most preferably of at least about 42°C. Varying additional parameters, such as hybridization time, the concentration of detergent, e.g., sodium dodecyl sulfate (SDS), and the inclusion or exclusion of carrier DNA, are well known to those skilled in the art. Various levels of stringency are accomplished by combining these various conditions as needed. In a preferred embodiment, hybridization will occur at 30°C in 750 mM NaCl, 75 mM trisodium citrate, and 1% SDS. In a more preferred embodiment, hybridization will occur at 37°C in 500 mM NaCl, 50 mM trisodium citrate, 1% SDS, 35% 30 formamide, and 100 µg/ml denatured salmon sperm DNA (ssDNA). In a most preferred embodiment, hybridization will occur at 42°C in 250 mM NaCl, 25 mM trisodium citrate, 1% SDS, 50 % formamide, and 200 μ g/ml ssDNA. Useful variations on these conditions will be readily apparent to those skilled in the art.

The washing steps which follow hybridization can also vary in stringency. Wash stringency conditions can be defined by salt concentration and by temperature. As above, wash stringency can

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be increased by decreasing salt concentration or by increasing temperature. For example, stringent salt concentration for the wash steps will preferably be less than about 30 mM NaCl and 3 mM trisodium citrate, and most preferably less than about 15 mM NaCl and 1.5 mM trisodium citrate. Stringent temperature conditions for the wash steps will ordinarily include temperature of at least about 25°C, more preferably of at least about 42°C, and most preferably of at least about 68°C. In a preferred embodiment, wash steps will occur at 25°C in 30 mM NaCl, 3 mM trisodium citrate, and 0.1% SDS. In a more preferred embodiment, wash steps will occur at 42°C in 15 mM NaCl, 1.5 mM trisodium citrate, and 0.1% SDS. In a most preferred embodiment, wash steps will occur at 68°C in 15 mM NaCl, 1.5 mM trisodium citrate, and 0.1% SDS. Additional variations on these conditions will be readily apparent to those skilled in the art.

Methods for DNA sequencing are well known in the art and may be used to practice any of the embodiments of the invention. The methods may employ such enzymes as the Klenow fragment of DNA polymerase I, SEQUENASE (US Biochemical, Cleveland OH), Taq polymerase (Perkin-Elmer), thermostable T7 polymerase (Amersham Pharmacia Biotech, Piscataway NJ), or combinations of polymerases and proofreading exonucleases such as those found in the ELONGASE amplification system (Life Technologies, Gaithersburg MD). Preferably, sequence preparation is automated with machines such as the MICROLAB 2200 (Hamilton, Reno NV), Peltier thermal cycler 200 (PTC200; MJ Research, Watertown MA) and the ABI CATALYST 800 (Perkin-Elmer). Sequencing is then carried out using the ABI 373 or 377 DNA sequencing systems (Perkin-Elmer), or the MEGABACE 1000 DNA sequencing system (Molecular Dynamics, Sunnyvale CA), or other systems known in the art. The resulting sequences are analyzed using a variety of algorithms which are well known in the art. (See, e.g., Ausubel, F.M. (1997) Short Protocols in Molecular Biology, John Wiley & Sons, New York NY, unit 7.7; Meyers, R.A. (1995) Molecular Biology and Biotechnology, Wiley VCH, New York NY, pp. 856-853.)

The nucleic acid sequences encoding PHSP may be extended utilizing a partial nucleotide sequence and employing various PCR-based methods known in the art to detect upstream sequences, such as promoters and regulatory elements. For example, one method which may be employed, restriction-site PCR, uses universal and nested primers to amplify unknown sequence from genomic DNA within a cloning vector. (See, e.g., Sarkar, G. (1993) PCR Methods Applic. 2:318-322.)

Another method, inverse PCR, uses primers that extend in divergent directions to amplify unknown sequence from a circularized template. The template is derived from restriction fragments comprising a known genomic locus and surrounding sequences. (See, e.g., Triglia, T. et al. (1988) Nucleic Acids Res. 16:8186.) A third method, capture PCR, involves PCR amplification of DNA fragments adjacent to known sequences in human and yeast artificial chromosome DNA. (See, e.g., Lagerstrom, M. et al. (1991) PCR Methods Applic. 1:111-119.) In this method, multiple restriction enzyme digestions

and ligations may be used to insert an engineered double-stranded sequence into a region of unknown sequence before performing PCR. Other methods which may be used to retrieve unknown sequences are known in the art. (See, e.g., Parker, J.D. et al. (1991) Nucleic Acids Res. 19:3055-306). Additionally, one may use PCR, nested primers, and PROMOTERFINDER libraries (Clontech, Palo Alto CA) to walk genomic DNA. This procedure avoids the need to screen libraries and is useful in finding intron/exon junctions. For all PCR-based methods, primers may be designed using commercially available software, such as OLIGO 4.06 primer analysis software (National Biosciences, Plymouth MN) or another appropriate program, to be about 22 to 30 nucleotides in length, to have a GC content of about 50% or more, and to anneal to the template at temperatures of about 68°C to 72°C.

When screening for full-length cDNAs, it is preferable to use libraries that have been size-selected to include larger cDNAs. In addition, random-primed libraries, which often include sequences containing the 5' regions of genes, are preferable for situations in which an oligo d(T) library does not yield a full-length cDNA. Genomic libraries may be useful for extension of sequence into 5' non-transcribed regulatory regions.

Capillary electrophoresis systems which are commercially available may be used to analyze the size or confirm the nucleotide sequence of sequencing or PCR products. In particular, capillary sequencing may employ flowable polymers for electrophoretic separation, four different nucleotide-specific, laser-stimulated fluorescent dyes, and a charge coupled device camera for detection of the emitted wavelengths. Output/light intensity may be converted to electrical signal using appropriate software (e.g., GENOTYPER and SEQUENCENAVIGATOR, Perkin-Elmer), and the entire process from loading of samples to computer analysis and electronic data display may be computer controlled. Capillary electrophoresis is especially preferable for sequencing small DNA fragments which may be present in limited amounts in a particular sample.

In another embodiment of the invention, polynucleotide sequences or fragments thereof which encode PHSP may be cloned in recombinant DNA molecules that direct expression of PHSP, or fragments or functional equivalents thereof, in appropriate host cells. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be produced and used to express PHSP.

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The nucleotide sequences of the present invention can be engineered using methods generally known in the art in order to alter PHSP-encoding sequences for a variety of purposes including, but not limited to, modification of the cloning, processing, and/or expression of the gene product. DNA shuffling by random fragmentation and PCR reassembly of gene fragments and synthetic oligonucleotides may be used to engineer the nucleotide sequences. For example, oligonucleotide-mediated site-directed mutagenesis may be used to introduce mutations that create new restriction

sites, alter glycosylation patterns, change codon preference, produce splice variants, and so forth.

In another embodiment, sequences encoding PHSP may be synthesized, in whole or in part, using chemical methods well known in the art. (See, e.g., Caruthers, M.H. et al. (1980) Nucl. Acids Res. Symp. Ser. 215-223, and Horn, T. et al. (1980) Nucl. Acids Res. Symp. Ser. 225-232.)

5 Alternatively, PHSP itself or a fragment thereof may be synthesized using chemical methods. For example, peptide synthesis can be performed using various solid-phase techniques. (See, e.g., Roberge, J.Y. et al. (1995) Science 269:202-204.) Automated synthesis may be achieved using the ABI 431A Peptide Synthesizer (Perkin-Elmer). Additionally, the amino acid sequence of PHSP, or any part thereof, may be altered during direct synthesis and/or combined with sequences from other proteins, or any part thereof, to produce a variant polypeptide.

The peptide may be substantially purified by preparative high performance liquid chromatography. (See, e.g, Chiez, R.M. and F.Z. Regnier (1990) Methods Enzymol. 182:392-421.)

The composition of the synthetic peptides may be confirmed by amino acid analysis or by sequencing. (See, e.g., Creighton, T. (1984) Proteins, Structures and Molecular Properties, WH Freeman, New York NY.)

In order to express a biologically active PHSP, the nucleotide sequences encoding PHSP or derivatives thereof may be inserted into an appropriate expression vector, i.e., a vector which contains the necessary elements for transcriptional and translational control of the inserted coding sequence in a suitable host. These elements include regulatory sequences, such as enhancers, constitutive and 20 inducible promoters, and 5' and 3' untranslated regions in the vector and in polynucleotide sequences encoding PHSP. Such elements may vary in their strength and specificity. Specific initiation signals may also be used to achieve more efficient translation of sequences encoding PHSP. Such signals include the ATG initiation codon and adjacent sequences, e.g. the Kozak sequence. In cases where sequences encoding PHSP and its initiation codon and upstream regulatory sequences are inserted into 25 the appropriate expression vector, no additional transcriptional or translational control signals may be needed. However, in cases where only coding sequence, or a fragment thereof, is inserted, exogenous translational control signals including an in-frame ATG initiation codon should be provided by the vector. Exogenous translational elements and initiation codons may be of various origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of enhancers appropriate for the particular host cell system used. (See, e.g., Scharf, D. et al. (1994) Results Probl. Cell Differ. 20:125-162.)

Methods which are well known to those skilled in the art may be used to construct expression vectors containing sequences encoding PHSP and appropriate transcriptional and translational control elements. These methods include <u>in vitro</u> recombinant DNA techniques, synthetic techniques, and <u>in vivo</u> genetic recombination. (See, e.g., Sambrook, J. et al. (1989) <u>Molecular Cloning</u>, A <u>Laboratory</u>

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Manual, Cold Spring Harbor Press, Plainview NY, ch. 4, 8, and 16-17; Ausubel, F.M. et al. (1995) Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, ch. 9, 13, and 16.)

A variety of expression vector/host systems may be utilized to contain and express sequences encoding PHSP. These include, but are not limited to, microorganisms such as bacteria transformed with recombinant bacteriophage, plasmid, or cosmid DNA expression vectors; yeast transformed with yeast expression vectors; insect cell systems infected with viral expression vectors (e.g., baculovirus); plant cell systems transformed with viral expression vectors (e.g., cauliflower mosaic virus, CaMV, or tobacco mosaic virus, TMV) or with bacterial expression vectors (e.g., Ti or pBR322 plasmids); or animal cell systems. The invention is not limited by the host cell employed.

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In bacterial systems, a number of cloning and expression vectors may be selected depending upon the use intended for polynucleotide sequences encoding PHSP. For example, routine cloning, subcloning, and propagation of polynucleotide sequences encoding PHSP can be achieved using a multifunctional E. coli vector such as PBLUESCRIPT (Stratagene, La Jolla CA) or pSPORT1 plasmid (Life Technologies). Ligation of sequences encoding PHSP into the vector's multiple cloning site 15 disrupts the lacZ gene, allowing a colorimetric screening procedure for identification of transformed bacteria containing recombinant molecules. In addition, these vectors may be useful for in vitro transcription, dideoxy sequencing, single strand rescue with helper phage, and creation of nested deletions in the cloned sequence. (See, e.g., Van Heeke, G. and S.M. Schuster (1989) J. Biol. Chem. 264:5503-5509.) When large quantities of PHSP are needed, e.g. for the production of antibodies, 20 vectors which direct high level expression of PHSP may be used. For example, vectors containing the strong, inducible T5 or T7 bacteriophage promoter may be used.

Yeast expression systems may be used for production of PHSP. A number of vectors containing constitutive or inducible promoters, such as alpha factor, alcohol oxidase, and PGH, may be used in the yeast Saccharomyces cerevisiae or Pichia pastoris. In addition, such vectors direct either the secretion or intracellular retention of expressed proteins and enable integration of foreign sequences into the host genome for stable propagation. (See, e.g., Ausubel, 1995, supra; Grant et al. (1987) Methods Enzymol. 153:516-54; and Scorer, C. A. et al. (1994) Bio/Technology 12:181-184.)

Plant systems may also be used for expression of PHSP. Transcription of sequences encoding PHSP may be driven viral promoters, e.g., the 35S and 19S promoters of CaMV used alone or in 30 combination with the omega leader sequence from TMV (Takamatsu, N. (1987) EMBO J. 6:307-311). Alternatively, plant promoters such as the small subunit of RUBISCO or heat shock promoters may be used. (See, e.g., Coruzzi, G. et al. (1984) EMBO J. 3:1671-1680; Broglie, R. et al. (1984) Science 224:838-843; and Winter, J. et al. (1991) Results Probl. Cell Differ. 17:85-105.) These constructs can be introduced into plant cells by direct DNA transformation or pathogen-mediated transfection. (See, 35 e.g., The McGraw Hill Yearbook of Science and Technology (1992) McGraw Hill, New York NY,

pp. 191-196.)

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In mammalian cells, a number of viral-based expression systems may be utilized. In cases where an adenovirus is used as an expression vector, sequences encoding PHSP may be ligated into an adenovirus transcription/translation complex consisting of the late promoter and tripartite leader sequence. Insertion in a non-essential E1 or E3 region of the viral genome may be used to obtain infective virus which expresses PHSP in host cells. (See, e.g., Logan, J. and T. Shenk (1984) Proc. Natl. Acad. Sci. 81:3655-3659.) In addition, transcription enhancers, such as the Rous sarcoma virus (RSV) enhancer, may be used to increase expression in mammalian host cells. SV40 or EBV-based vectors may also be used for high-level protein expression.

Human artificial chromosomes (HACs) may also be employed to deliver larger fragments of DNA than can be contained in and expressed from a plasmid. HACs of about 6 kb to 10 Mb are constructed and delivered via conventional delivery methods (liposomes, polycationic amino polymers, or vesicles) for therapeutic purposes. (See, e.g., Harrington, J.J. et al. (1997) Nat Genet. 15:345-355.)

For long term production of recombinant proteins in mammalian systems, stable expression of PHSP in cell lines is preferred. For example, sequences encoding PHSP can be transformed into cell lines using expression vectors which may contain viral origins of replication and/or endogenous expression elements and a selectable marker gene on the same or on a separate vector. Following the introduction of the vector, cells may be allowed to grow for about 1 to 2 days in enriched media before being switched to selective media. The purpose of the selectable marker is to confer resistance to a selective agent, and its presence allows growth and recovery of cells which successfully express the introduced sequences. Resistant clones of stably transformed cells may be propagated using tissue culture techniques appropriate to the cell type.

Any number of selection systems may be used to recover transformed cell lines. These include, but are not limited to, the herpes simplex virus thymidine kinase and adenine phosphoribosyltransferase genes, for use in *tk* or *apr* cells, respectively. (See, e.g., Wigler, M. et al. (1977) Cell 11:223-232; Lowy, I. et al. (1980) Cell 22:817-823.) Also, antimetabolite, antibiotic, or herbicide resistance can be used as the basis for selection. For example, *dhfr* confers resistance to methotrexate; *neo* confers resistance to the aminoglycosides, neomycin and G-418; and *als* or *pat* confer resistance to chlorsulfuron and phosphinotricin acetyltransferase, respectively. (See, e.g., Wigler, M. et al. (1980) Proc. Natl. Acad. Sci. 77:3567-3570; Colbere-Garapin, F. et al. (1981) J. Mol. Biol. 150:1-14.) Additional selectable genes have been described, e.g., *trpB* and *hisD*, which alter cellular requirements for metabolites. (See, e.g., Hartman, S.C. and R.C. Mulligan (1988) Proc. Natl. Acad. Sci. 85:8047-8051.) Visible markers, e.g., anthocyanins, green fluorescent proteins (GFP; Clontech), ß glucuronidase and its substrate ß-glucuronide, or luciferase and its substrate luciferin may

be used. These markers can be used not only to identify transformants, but also to quantify the amount of transient or stable protein expression attributable to a specific vector system. (See, e.g., Rhodes, C.A. (1995) Methods Mol. Biol. 55:121-131.)

Although the presence/absence of marker gene expression suggests that the gene of interest is also present, the presence and expression of the gene may need to be confirmed. For example, if the sequence encoding PHSP is inserted within a marker gene sequence, transformed cells containing sequences encoding PHSP can be identified by the absence of marker gene function. Alternatively, a marker gene can be placed in tandem with a sequence encoding PHSP under the control of a single promoter. Expression of the marker gene in response to induction or selection usually indicates expression of the tandem gene as well.

In general, host cells that contain the nucleic acid sequence encoding PHSP and that express PHSP may be identified by a variety of procedures known to those of skill in the art. These procedures include, but are not limited to, DNA-DNA or DNA-RNA hybridizations, PCR amplification, and protein bioassay or immunoassay techniques which include membrane, solution, or chip based technologies for the detection and/or quantification of nucleic acid or protein sequences.

Immunological methods for detecting and measuring the expression of PHSP using either specific polyclonal or monoclonal antibodies are known in the art. Examples of such techniques include enzyme-linked immunosorbent assays (ELISAs), radioimmunoassays (RIAs), and fluorescence activated cell sorting (FACS). A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering epitopes on PHSP is preferred, but a competitive binding assay may be employed. These and other assays are well known in the art. (See, e.g., Hampton, R. et al. (1990) Serological Methods, a Laboratory Manual, APS Press, St Paul MN, Sect. IV; Coligan, J. E. et al. (1997) Current Protocols in Immunology, Greene Pub. Associates and Wiley-Interscience, New York NY; and Pound, J.D. (1998) Immunochemical Protocols, Humana Press, Totowa NJ).

A wide variety of labels and conjugation techniques are known by those skilled in the art and may be used in various nucleic acid and amino acid assays. Means for producing labeled hybridization or PCR probes for detecting sequences related to polynucleotides encoding PHSP include oligolabeling, nick translation, end-labeling, or PCR amplification using a labeled nucleotide.

30 Alternatively, the sequences encoding PHSP, or any fragments thereof, may be cloned into a vector for the production of an mRNA probe. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes in vitro by addition of an appropriate RNA polymerase such as T7, T3, or SP6 and labeled nucleotides. These procedures may be conducted using a variety of commercially available kits, such as those provided by Amersham Pharmacia Biotech, Promega (Madison WI), and US Biochemical. Suitable reporter molecules or labels which may be used for

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ease of detection include radionuclides, enzymes, fluorescent, chemiluminescent, or chromogenic agents, as well as substrates, cofactors, inhibitors, magnetic particles, and the like.

Host cells transformed with nucleotide sequences encoding PHSP may be cultured under conditions suitable for the expression and recovery of the protein from cell culture. The protein produced by a transformed cell may be secreted or retained intracellularly depending on the sequence and/or the vector used. As will be understood by those of skill in the art, expression vectors containing polynucleotides which encode PHSP may be designed to contain signal sequences which direct secretion of PHSP through a prokaryotic or eukaryotic cell membrane.

In addition, a host cell strain may be chosen for its ability to modulate expression of the inserted sequences or to process the expressed protein in the desired fashion. Such modifications of the polypeptide include, but are not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation, and acylation. Post-translational processing which cleaves a "prepro" form of the protein may also be used to specify protein targeting, folding, and/or activity. Different host cells which have specific cellular machinery and characteristic mechanisms for post-translational activities (e.g., CHO, HeLa, MDCK, HEK293, and WI38), are available from the American Type Culture Collection (ATCC, Bethesda MD) and may be chosen to ensure the correct modification and processing of the foreign protein.

In another embodiment of the invention, natural, modified, or recombinant nucleic acid sequences encoding PHSP may be ligated to a heterologous sequence resulting in translation of a 20 fusion protein in any of the aforementioned host systems. For example, a chimeric PHSP protein containing a heterologous moiety that can be recognized by a commercially available antibody may facilitate the screening of peptide libraries for inhibitors of PHSP activity. Heterologous protein and peptide moieties may also facilitate purification of fusion proteins using commercially available affinity matrices. Such moieties include, but are not limited to, glutathione S-transferase (GST), maltose binding protein (MBP), thioredoxin (Trx), calmodulin binding peptide (CBP), 6-His, FLAG, c-myc, and hemagglutinin (HA). GST, MBP, Trx, CBP, and 6-His enable purification of their cognate fusion proteins on immobilized glutathione, maltose, phenylarsine oxide, calmodulin, and metalchelate resins, respectively. FLAG, c-myc, and hemagglutinin (HA) enable immunoaffinity purification of fusion proteins using commercially available monoclonal and polyclonal antibodies 30 that specifically recognize these epitope tags. A fusion protein may also be engineered to contain a proteolytic cleavage site located between the PHSP encoding sequence and the heterologous protein sequence, so that PHSP may be cleaved away from the heterologous moiety following purification. Methods for fusion protein expression and purification are discussed in Ausubel (1995, supra, ch 10). A variety of commercially available kits may also be used to facilitate expression and purification of fusion proteins.

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In a further embodiment of the invention, synthesis of radiolabeled PHSP may be achieved in vitro using the TNT rabbit reticulocyte lysate or wheat germ extract systems (Promega). These systems couple transcription and translation of protein-coding sequences operably associated with the T7, T3, or SP6 promoters. Translation takes place in the presence of a radiolabeled amino acid precursor, preferably ³⁵S-methionine.

Fragments of PHSP may be produced not only by recombinant production, but also by direct peptide synthesis using solid-phase techniques. (See, e.g., Creighton, supra, pp. 55-60.) Protein synthesis may be performed by manual techniques or by automation. Automated synthesis may be achieved, for example, using the ABI 431A Peptide Synthesizer (Perkin-Elmer). Various fragments 10 of PHSP may be synthesized separately and then combined to produce the full length molecule.

THERAPEUTICS

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Chemical and structural similarity, e.g., in the context of sequences and motifs, exists between regions of PHSP and protein phosphatases. In addition, the expression of PHSP is closely associated with reproductive tissue, nervous tissue, gastrointestinal tissue, cell proliferation, cancer, 15 inflammation, and immune response. Therefore, PHSP appears to play a role in cell proliferative, immune, and neuronal disorders. In the treatment of disorders associated with increased PHSP expression or activity, it is desirable to decrease the expression or activity of PHSP. In the treatment of disorders associated with decreased PHSP expression or activity, it is desirable to increase the expression or activity of PHSP.

Therefore, in one embodiment, PHSP or a fragment or derivative thereof may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of PHSP. Examples of such disorders include, but are not limited to, a cell proliferative disorder, such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal hemoglobinuria, polycythemia vera, psoriasis, primary 25 thrombocythemia, and cancers including adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus; an immune disorder, such as acquired immunodeficiency syndrome (AIDS), 30 Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anemia, asthma, atherosclerosis, autoimmune hemolytic anemia, autoimmune thyroiditis, autoimmune polyenodocrinopathy-candidiasis-ectodermal dystrophy (APECED), bronchitis, cholecystitis, contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, episodic lymphopenia with lymphocytotoxins, erythroblastosis fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis,

hypereosinophilia, irritable bowel syndrome, multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, osteoarthritis, osteoporosis, pancreatitis, polymyositis, psoriasis, Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjögren's syndrome, systemic anaphylaxis, systemic lupus erythematosus, systemic sclerosis, thrombocytopenic purpura, ulcerative colitis, uveitis, Werner syndrome, complications of cancer, hemodialysis, and extracorporeal circulation, viral, bacterial, fungal, parasitic, protozoal, and helminthic infections, and trauma; and a neuronal disorder, such as akathesia, Alzheimer's disease, amnesia, amyotrophic lateral sclerosis, bipolar disorder, catatonia, dementia, depression, diabetic neuropathy, Down's syndrome, tardive dyskinesia, dystonias, epilepsy, Huntington's disease, peripheral neuropathy, multiple sclerosis, neurofibromatosis, Parkinson's disease, paranoid psychoses, postherpetic neuralgia, schizophrenia, and Tourette's disorder.

In another embodiment, a vector capable of expressing PHSP or a fragment or derivative thereof may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of PHSP including, but not limited to, those described above.

In a further embodiment, a pharmaceutical composition comprising a substantially purified
PHSP in conjunction with a suitable pharmaceutical carrier may be administered to a subject to treat
or prevent a disorder associated with decreased expression or activity of PHSP including, but not
limited to, those provided above.

In still another embodiment, an agonist which modulates the activity of PHSP may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of PHSP including, but not limited to, those listed above.

In a further embodiment, an antagonist of PHSP may be administered to a subject to treat or prevent a disorder associated with increased expression or activity of PHSP. Examples of such disorders include, but are not limited to, those described above. In one aspect, an antibody which specifically binds PHSP may be used directly as an antagonist or indirectly as a targeting or delivery mechanism for bringing a pharmaceutical agent to cells or tissue which express PHSP.

In an additional embodiment, a vector expressing the complement of the polynucleotide encoding PHSP may be administered to a subject to treat or prevent a disorder associated with increased expression or activity of PHSP including, but not limited to, those described above.

In other embodiments, any of the proteins, antagonists, antibodies, agonists, complementary sequences, or vectors of the invention may be administered in combination with other appropriate therapeutic agents. Selection of the appropriate agents for use in combination therapy may be made by one of ordinary skill in the art, according to conventional pharmaceutical principles. The combination of therapeutic agents may act synergistically to effect the treatment or prevention of the various disorders described above. Using this approach, one may be able to achieve therapeutic efficacy with lower dosages of each agent, thus reducing the potential for adverse side effects.

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An antagonist of PHSP may be produced using methods which are generally known in the art. In particular, purified PHSP may be used to produce antibodies or to screen libraries of pharmaceutical agents to identify those which specifically bind PHSP. Antibodies to PHSP may also be generated using methods that are well known in the art. Such antibodies may include, but are not limited to, polyclonal, monoclonal, chimeric, and single chain antibodies, Fab fragments, and fragments produced by a Fab expression library. Neutralizing antibodies (i.e., those which inhibit dimer formation) are especially preferred for therapeutic use.

For the production of antibodies, various hosts including goats, rabbits, rats, mice, humans, and others may be immunized by injection with PHSP or with any fragment or oligopeptide thereof which has immunogenic properties. Depending on the host species, various adjuvants may be used to increase immunological response. Such adjuvants include, but are not limited to, Freund's, mineral gels such as aluminum hydroxide, and surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, KLH, and dinitrophenol. Among adjuvants used in humans, BCG (bacilli Calmette-Guerin) and Corynebacterium parvum are especially preferable.

It is preferred that the oligopeptides, peptides, or fragments used to induce antibodies to PHSP have an amino acid sequence consisting of at least about 5 amino acids, and, more preferably, of at least about 10 amino acids. It is also preferable that these oligopeptides, peptides, or fragments are identical to a portion of the amino acid sequence of the natural protein and contain the entire amino acid sequence of a small, naturally occurring molecule. Short stretches of PHSP amino acids may be fused with those of another protein, such as KLH, and antibodies to the chimeric molecule may be produced.

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Monoclonal antibodies to PHSP may be prepared using any technique which provides for the production of antibody molecules by continuous cell lines in culture. These include, but are not limited to, the hybridoma technique, the human B-cell hybridoma technique, and the EBV-hybridoma technique. (See, e.g., Kohler, G. et al. (1975) Nature 256:495-497; Kozbor, D. et al. (1985) J. Immunol. Methods 81:31-42; Cote, R.J. et al. (1983) Proc. Natl. Acad. Sci. 80:2026-2030; and Cole, S.P. et al. (1984) Mol. Cell Biol. 62:109-120.)

In addition, techniques developed for the production of "chimeric antibodies," such as the splicing of mouse antibody genes to human antibody genes to obtain a molecule with appropriate antigen specificity and biological activity, can be used. (See, e.g., Morrison, S.L. et al. (1984) Proc. Natl. Acad. Sci. 81:6851-6855; Neuberger, M.S. et al. (1984) Nature 312:604-608; and Takeda, S. et al. (1985) Nature 314:452-454.) Alternatively, techniques described for the production of single chain antibodies may be adapted, using methods known in the art, to produce PHSP-specific single chain antibodies. Antibodies with related specificity, but of distinct idiotypic composition, may be generated by chain shuffling from random combinatorial immunoglobulin libraries. (See, e.g., Burton

D.R. (1991) Proc. Natl. Acad. Sci. 88:10134-10137.)

Antibodies may also be produced by inducing <u>in vivo</u> production in the lymphocyte population or by screening immunoglobulin libraries or panels of highly specific binding reagents as disclosed in the literature. (See, e.g., Orlandi, R. et al. (1989) Proc. Natl. Acad. Sci. 86: 3833-3837; Winter, G. et al. (1991) Nature 349:293-299.)

Antibody fragments which contain specific binding sites for PHSP may also be generated. For example, such fragments include, but are not limited to, F(ab')2 fragments produced by pepsin digestion of the antibody molecule and Fab fragments generated by reducing the disulfide bridges of the F(ab')2 fragments. Alternatively, Fab expression libraries may be constructed to allow rapid and easy identification of monoclonal Fab fragments with the desired specificity. (See, e.g., Huse, W.D. et al. (1989) Science 246:1275-1281.)

Various immunoassays may be used for screening to identify antibodies having the desired specificity. Numerous protocols for competitive binding or immunoradiometric assays using either polyclonal or monoclonal antibodies with established specificities are well known in the art. Such immunoassays typically involve the measurement of complex formation between PHSP and its specific antibody. A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering PHSP epitopes is preferred, but a competitive binding assay may also be employed (Pound, supra).

Various methods such as Scatchard analysis in conjunction with radioimmunoassay techniques may be used to assess the affinity of antibodies for PHSP. Affinity is expressed as an association constant, K_a, which is defined as the molar concentration of PHSP-antibody complex divided by the molar concentrations of free antigen and free antibody under equilibrium conditions. The K_a determined for a preparation of polyclonal antibodies, which are heterogeneous in their affinities for multiple PHSP epitopes, represents the average affinity, or avidity, of the antibodies for PHSP. The K_a determined for a preparation of monoclonal antibodies, which are monospecific for a particular PHSP epitope, represents a true measure of affinity. High-affinity antibody preparations with K_a ranging from about 10° to 10¹² L/mole are preferred for use in immunoassays in which the PHSP-antibody complex must withstand rigorous manipulations. Low-affinity antibody preparations with K_a ranging from about 10° to 10¹ L/mole are preferred for use in immunopurification and similar procedures which ultimately require dissociation of PHSP, preferably in active form, from the antibody (Catty, D. (1988) Antibodies, Volume I: A Practical Approach, IRL Press, Washington, DC; Liddell, J. E. and Cryer, A. (1991) A Practical Guide to Monoclonal Antibodies, John Wiley & Sons, New York NY).

The titer and avidity of polyclonal antibody preparations may be further evaluated to determine the quality and suitability of such preparations for certain downstream applications. For

example, a polyclonal antibody preparation containing at least 1-2 mg specific antibody/ml, preferably 5-10 mg specific antibody/ml, is preferred for use in procedures requiring precipitation of PHSP-antibody complexes. Procedures for evaluating antibody specificity, titer, and avidity, and guidelines for antibody quality and usage in various applications, are generally available. (See, e.g., Catty, supra, and Coligan et al. supra.)

In another embodiment of the invention, the polynucleotides encoding PHSP, or any fragment or complement thereof, may be used for therapeutic purposes. In one aspect, the complement of the polynucleotide encoding PHSP may be used in situations in which it would be desirable to block the transcription of the mRNA. In particular, cells may be transformed with sequences complementary to polynucleotides encoding PHSP. Thus, complementary molecules or fragments may be used to modulate PHSP activity, or to achieve regulation of gene function. Such technology is now well known in the art, and sense or antisense oligonucleotides or larger fragments can be designed from various locations along the coding or control regions of sequences encoding PHSP.

Expression vectors derived from retroviruses, adenoviruses, or herpes or vaccinia viruses, or from various bacterial plasmids, may be used for delivery of nucleotide sequences to the targeted organ, tissue, or cell population. Methods which are well known to those skilled in the art can be used to construct vectors to express nucleic acid sequences complementary to the polynucleotides encoding PHSP. (See, e.g., Sambrook, <u>supra</u>; Ausubel, 1995, <u>supra</u>.)

Genes encoding PHSP can be turned off by transforming a cell or tissue with expression vectors which express high levels of a polynucleotide, or fragment thereof, encoding PHSP. Such constructs may be used to introduce untranslatable sense or antisense sequences into a cell. Even in the absence of integration into the DNA, such vectors may continue to transcribe RNA molecules until they are disabled by endogenous nucleases. Transient expression may last for a month or more with a non-replicating vector, and may last even longer if appropriate replication elements are part of the vector system.

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As mentioned above, modifications of gene expression can be obtained by designing complementary sequences or antisense molecules (DNA, RNA, or PNA) to the control, 5', or regulatory regions of the gene encoding PHSP. Oligonucleotides derived from the transcription initiation site, e.g., between about positions -10 and +10 from the start site, are preferred. Similarly, inhibition can be achieved using triple helix base-pairing methodology. Triple helix pairing is useful because it causes inhibition of the ability of the double helix to open sufficiently for the binding of polymerases, transcription factors, or regulatory molecules. Recent therapeutic advances using triplex DNA have been described in the literature. (See, e.g., Gee, J.E. et al. (1994) in Huber, B.E. and B.I. Carr, Molecular and Immunologic Approaches, Futura Publishing, Mt. Kisco NY, pp. 163-177.) A complementary sequence or antisense molecule may also be designed to block translation of mRNA

by preventing the transcript from binding to ribosomes.

Ribozymes, enzymatic RNA molecules, may also be used to catalyze the specific cleavage of RNA. The mechanism of ribozyme action involves sequence-specific hybridization of the ribozyme molecule to complementary target RNA, followed by endonucleolytic cleavage. For example, engineered hammerhead motif ribozyme molecules may specifically and efficiently catalyze endonucleolytic cleavage of sequences encoding PHSP.

Specific ribozyme cleavage sites within any potential RNA target are initially identified by scanning the target molecule for ribozyme cleavage sites, including the following sequences: GUA, GUU, and GUC. Once identified, short RNA sequences of between 15 and 20 ribonucleotides, corresponding to the region of the target gene containing the cleavage site, may be evaluated for secondary structural features which may render the oligonucleotide inoperable. The suitability of candidate targets may also be evaluated by testing accessibility to hybridization with complementary oligonucleotides using ribonuclease protection assays.

Complementary ribonucleic acid molecules and ribozymes of the invention may be prepared by any method known in the art for the synthesis of nucleic acid molecules. These include techniques for chemically synthesizing oligonucleotides such as solid phase phosphoramidite chemical synthesis. Alternatively, RNA molecules may be generated by in vitro and in vivo transcription of DNA sequences encoding PHSP. Such DNA sequences may be incorporated into a wide variety of vectors with suitable RNA polymerase promoters such as T7 or SP6. Alternatively, these cDNA constructs that synthesize complementary RNA, constitutively or inducibly, can be introduced into cell lines, cells, or tissues.

RNA molecules may be modified to increase intracellular stability and half-life. Possible modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3' ends of the molecule, or the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages within the backbone of the molecule. This concept is inherent in the production of PNAs and can be extended in all of these molecules by the inclusion of nontraditional bases such as inosine, queosine, and wybutosine, as well as acetyl-, methyl-, thio-, and similarly modified forms of adenine, cytidine, guanine, thymine, and uridine which are not as easily recognized by endogenous endonucleases.

Many methods for introducing vectors into cells or tissues are available and equally suitable for use in vivo, in vitro, and ex vivo. For ex vivo therapy, vectors may be introduced into stem cells taken from the patient and clonally propagated for autologous transplant back into that same patient. Delivery by transfection, by liposome injections, or by polycationic amino polymers may be achieved using methods which are well known in the art. (See, e.g., Goldman, C.K. et al. (1997) Nature Biotechnology 15:462-466.)

35 Any of the therapeutic methods described above may be applied to any subject in need of such

therapy, including, for example, mammals such as dogs, cats, cows, horses, rabbits, monkeys, and most preferably, humans.

An additional embodiment of the invention relates to the administration of a pharmaceutical or sterile composition, in conjunction with a pharmaceutically acceptable carrier, for any of the therapeutic effects discussed above. Such pharmaceutical compositions may consist of PHSP, antibodies to PHSP, and mimetics, agonists, antagonists, or inhibitors of PHSP. The compositions may be administered alone or in combination with at least one other agent, such as a stabilizing compound, which may be administered in any sterile, biocompatible pharmaceutical carrier including, but not limited to, saline, buffered saline, dextrose, and water. The compositions may be administered to a patient alone, or in combination with other agents, drugs, or hormones.

The pharmaceutical compositions utilized in this invention may be administered by any number of routes including, but not limited to, oral, intravenous, intramuscular, intra-arterial, intramedullary, intrathecal, intraventricular, transdermal, subcutaneous, intraperitoneal, intranasal, enteral, topical, sublingual, or rectal means.

In addition to the active ingredients, these pharmaceutical compositions may contain suitable pharmaceutically-acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. Further details on techniques for formulation and administration may be found in the latest edition of <u>Remington's Pharmaceutical Sciences</u> (Maack Publishing, Easton PA).

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Pharmaceutical compositions for oral administration can be formulated using pharmaceutically acceptable carriers well known in the art in dosages suitable for oral administration. Such carriers enable the pharmaceutical compositions to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions, and the like, for ingestion by the patient.

Pharmaceutical preparations for oral use can be obtained through combining active compounds with solid excipient and processing the resultant mixture of granules (optionally, after grinding) to obtain tablets or dragee cores. Suitable auxiliaries can be added, if desired. Suitable excipients include carbohydrate or protein fillers, such as sugars, including lactose, sucrose, mannitol, and sorbitol; starch from corn, wheat, rice, potato, or other plants; cellulose, such as methyl cellulose, hydroxypropylmethyl-cellulose, or sodium carboxymethylcellulose; gums, including arabic and tragacanth; and proteins, such as gelatin and collagen. If desired, disintegrating or solubilizing agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, and alginic acid or a salt thereof, such as sodium alginate.

Dragee cores may be used in conjunction with suitable coatings, such as concentrated sugar solutions, which may also contain gum arabic, talc, polyvinylpyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures.

Dyestuffs or pigments may be added to the tablets or dragee coatings for product identification or to characterize the quantity of active compound, i.e., dosage.

Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a coating, such as glycerol or sorbitol. Push-fit capsules can contain active ingredients mixed with fillers or binders, such as lactose or starches, lubricants, such as talc or magnesium stearate, and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid, or liquid polyethylene glycol with or without stabilizers.

Pharmaceutical formulations suitable for parenteral administration may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks' solution, Ringer's solution, or physiologically buffered saline. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils, such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate, triglycerides, or liposomes. Non-lipid polycationic amino polymers may also be used for delivery. Optionally, the suspension may also contain suitable stabilizers or agents to increase the solubility of the compounds and allow for the preparation of highly concentrated solutions.

For topical or nasal administration, penetrants appropriate to the particular barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

The pharmaceutical compositions of the present invention may be manufactured in a manner that is known in the art, e.g., by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping, or lyophilizing processes.

The pharmaceutical composition may be provided as a salt and can be formed with many acids, including but not limited to, hydrochloric, sulfuric, acetic, lactic, tartaric, malic, and succinic acid. Salts tend to be more soluble in aqueous or other protonic solvents than are the corresponding free base forms. In other cases, the preferred preparation may be a lyophilized powder which may contain any or all of the following: 1 mM to 50 mM histidine, 0.1% to 2% sucrose, and 2% to 7% mannitol, at a pH range of 4.5 to 5.5, that is combined with buffer prior to use.

After pharmaceutical compositions have been prepared, they can be placed in an appropriate container and labeled for treatment of an indicated condition. For administration of PHSP, such labeling would include amount, frequency, and method of administration.

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Pharmaceutical compositions suitable for use in the invention include compositions wherein the active ingredients are contained in an effective amount to achieve the intended purpose. The determination of an effective dose is well within the capability of those skilled in the art.



For any compound, the therapeutically effective dose can be estimated initially either in cell culture assays, e.g., of neoplastic cells or in animal models such as mice, rats, rabbits, dogs, or pigs. An animal model may also be used to determine the appropriate concentration range and route of administration. Such information can then be used to determine useful doses and routes for administration in humans.

A therapeutically effective dose refers to that amount of active ingredient, for example PHSP or fragments thereof, antibodies of PHSP, and agonists, antagonists or inhibitors of PHSP, which ameliorates the symptoms or condition. Therapeutic efficacy and toxicity may be determined by standard pharmaceutical procedures in cell cultures or with experimental animals, such as by calculating the ED₅₀ (the dose therapeutically effective in 50% of the population) or LD₅₀ (the dose lethal to 50% of the population) statistics. The dose ratio of toxic to therapeutic effects is the therapeutic index, which can be expressed as the LD₅₀/ED₅₀ ratio. Pharmaceutical compositions which exhibit large therapeutic indices are preferred. The data obtained from cell culture assays and animal studies are used to formulate a range of dosage for human use. The dosage contained in such compositions is preferably within a range of circulating concentrations that includes the ED₅₀ with little or no toxicity. The dosage varies within this range depending upon the dosage form employed, the sensitivity of the patient, and the route of administration.

The exact dosage will be determined by the practitioner, in light of factors related to the subject requiring treatment. Dosage and administration are adjusted to provide sufficient levels of the active moiety or to maintain the desired effect. Factors which may be taken into account include the severity of the disease state, the general health of the subject, the age, weight, and gender of the subject, time and frequency of administration, drug combination(s), reaction sensitivities, and response to therapy. Long-acting pharmaceutical compositions may be administered every 3 to 4 days, every week, or biweekly depending on the half-life and clearance rate of the particular formulation.

Normal dosage amounts may vary from about $0.1~\mu g$ to $100,000~\mu g$, up to a total dose of about 1 gram, depending upon the route of administration. Guidance as to particular dosages and methods of delivery is provided in the literature and generally available to practitioners in the art. Those skilled in the art will employ different formulations for nucleotides than for proteins or their inhibitors. Similarly, delivery of polynucleotides or polypeptides will be specific to particular cells, conditions, locations, etc.

DIAGNOSTICS

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In another embodiment, antibodies which specifically bind PHSP may be used for the diagnosis of disorders characterized by expression of PHSP, or in assays to monitor patients being treated with PHSP or agonists, antagonists, or inhibitors of PHSP. Antibodies useful for diagnostic

purposes may be prepared in the same manner as described above for therapeutics. Diagnostic assays for PHSP include methods which utilize the antibody and a label to detect PHSP in human body fluids or in extracts of cells or tissues. The antibodies may be used with or without modification, and may be labeled by covalent or non-covalent attachment of a reporter molecule. A wide variety of reporter molecules, several of which are described above, are known in the art and may be used.

A variety of protocols for measuring PHSP, including ELISAs, RIAs, and FACS, are known in the art and provide a basis for diagnosing altered or abnormal levels of PHSP expression. Normal or standard values for PHSP expression are established by combining body fluids or cell extracts taken $from \, normal \, mammalian \, subjects, \, preferably \, human, \, with \, antibody \, to \, PHSP \, under \, conditions \, suitable \, and \, the subjects \, are the subjects and the subjects \, are the subjects and the subjects \, are the subjects \, and \, the subjects \, are the subject \, are the subjects \, are the subjects \, are the subjects \, are the subjects \, are the subject \, are the su$ for complex formation. The amount of standard complex formation may be quantitated by various methods, preferably by photometric means. Quantities of PHSP expressed in subject, control, and disease samples from biopsied tissues are compared with the standard values. Deviation between standard and subject values establishes the parameters for diagnosing disease.

In another embodiment of the invention, the polynucleotides encoding PHSP may be used for diagnostic purposes. The polynucleotides which may be used include oligonucleotide sequences, complementary RNA and DNA molecules, and PNAs. The polynucleotides may be used to detect and quantitate gene expression in biopsied tissues in which expression of PHSP may be correlated with disease. The diagnostic assay may be used to determine absence, presence, and excess expression of PHSP, and to monitor regulation of PHSP levels during therapeutic intervention.

In one aspect, hybridization with PCR probes which are capable of detecting polynucleotide sequences, including genomic sequences, encoding PHSP or closely related molecules may be used to identify nucleic acid sequences which encode PHSP. The specificity of the probe, whether it is made from a highly specific region, e.g., the 5' regulatory region, or from a less specific region, e.g., a conserved motif, and the stringency of the hybridization or amplification (maximal, high, 25 intermediate, or low), will determine whether the probe identifies only naturally occurring sequences encoding PHSP, allelic variants, or related sequences.

Probes may also be used for the detection of related sequences, and should preferably have at least 50% sequence identity to any of the PHSP encoding sequences. The hybridization probes of the subject invention may be DNA or RNA and may be derived from the sequence of SEQ ID NO:32-62 or from genomic sequences including promoters, enhancers, and introns of the PHSP gene.

Means for producing specific hybridization probes for DNAs encoding PHSP include the cloning of polynucleotide sequences encoding PHSP or PHSP derivatives into vectors for the production of mRNA probes. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes in vitro by means of the addition of the appropriate RNA polymerases and the appropriate labeled nucleotides. Hybridization probes may be labeled by a

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variety of reporter groups, for example, by radionuclides such as ³²P or ³⁵S, or by enzymatic labels, such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems, and the like.

Polynucleotide sequences encoding PHSP may be used for the diagnosis of disorders associated with expression of PHSP. Examples of such disorders include, but are not limited to, a cell proliferative disorder, such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal hemoglobinuria, polycythemia vera, psoriasis, primary thrombocythemia, and cancers including adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus; an immune disorder, such as acquired immunodeficiency syndrome (AIDS), Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anemia, asthma, atherosclerosis, autoimmune hemolytic anemia, autoimmune thyroiditis, autoimmune polyenodocrinopathy-15 candidiasis-ectodermal dystrophy (APECED), bronchitis, cholecystitis, contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, episodic lymphopenia with lymphocytotoxins, erythroblastosis fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, hypereosinophilia, irritable bowel syndrome, multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, osteoarthritis, osteoporosis, pancreatitis, polymyositis, psoriasis, Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjögren's syndrome, systemic anaphylaxis, systemic lupus erythematosus, systemic sclerosis, thrombocytopenic purpura, ulcerative colitis, uveitis, Werner syndrome, complications of cancer, hemodialysis, and extracorporeal circulation, viral, bacterial, fungal, parasitic, protozoal, and helminthic infections, and trauma; and a neuronal disorder, such as akathesia, Alzheimer's disease, amnesia, amyotrophic lateral sclerosis, bipolar disorder, catatonia, dementia, depression, diabetic neuropathy, Down's syndrome, tardive dyskinesia, dystonias, epilepsy, Huntington's disease, peripheral neuropathy, multiple sclerosis, neurofibromatosis, Parkinson's disease, paranoid psychoses, postherpetic neuralgia, schizophrenia, and Tourette's disorder. The polynucleotide sequences encoding PHSP may be used in Southern or northern analysis, dot blot, or other membrane-based technologies; in PCR technologies; in dipstick, pin, and multiformat ELISAlike assays; and in microarrays utilizing fluids or tissues from patients to detect altered PHSP expression. Such qualitative or quantitative methods are well known in the art.

In a particular aspect, the nucleotide sequences encoding PHSP may be useful in assays that detect the presence of associated disorders, particularly those mentioned above. The nucleotide sequences encoding PHSP may be labeled by standard methods and added to a fluid or tissue sample

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from a patient under conditions suitable for the formation of hybridization complexes. After a suitable incubation period, the sample is washed and the signal is quantitated and compared with a standard value. If the amount of signal in the patient sample is significantly altered in comparison to a control sample then the presence of altered levels of nucleotide sequences encoding PHSP in the sample indicates the presence of the associated disorder. Such assays may also be used to evaluate the efficacy of a particular therapeutic treatment regimen in animal studies, in clinical trials, or to monitor the treatment of an individual patient.

In order to provide a basis for the diagnosis of a disorder associated with expression of PHSP, a normal or standard profile for expression is established. This may be accomplished by combining 10 body fluids or cell extracts taken from normal subjects, either animal or human, with a sequence, or a fragment thereof, encoding PHSP, under conditions suitable for hybridization or amplification. Standard hybridization may be quantified by comparing the values obtained from normal subjects with values from an experiment in which a known amount of a substantially purified polynucleotide is used. Standard values obtained in this manner may be compared with values obtained from samples from patients who are symptomatic for a disorder. Deviation from standard values is used to establish the presence of a disorder.

Once the presence of a disorder is established and a treatment protocol is initiated, hybridization assays may be repeated on a regular basis to determine if the level of expression in the patient begins to approximate that which is observed in the normal subject. The results obtained from 20 successive assays may be used to show the efficacy of treatment over a period ranging from several days to months.

With respect to cancer, the presence of an abnormal amount of transcript (either under- or overexpressed) in biopsied tissue from an individual may indicate a predisposition for the development of the disease, or may provide a means for detecting the disease prior to the appearance of actual clinical symptoms. A more definitive diagnosis of this type may allow health professionals to employ preventative measures or aggressive treatment earlier thereby preventing the development or further progression of the cancer.

Additional diagnostic uses for oligonucleotides designed from the sequences encoding PHSP may involve the use of PCR. These oligomers may be chemically synthesized, generated 30 enzymatically, or produced in vitro. Oligomers will preferably contain a fragment of a polynucleotide encoding PHSP, or a fragment of a polynucleotide complementary to the polynucleotide encoding PHSP, and will be employed under optimized conditions for identification of a specific gene or condition. Oligomers may also be employed under less stringent conditions for detection or quantitation of closely related DNA or RNA sequences.

Methods which may also be used to quantify the expression of PHSP include radiolabeling

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or biotinylating nucleotides, coamplification of a control nucleic acid, and interpolating results from standard curves. (See, e.g., Melby, P.C. et al. (1993) J. Immunol. Methods 159:235-244; Duplaa, C. et al. (1993) Anal. Biochem. 212:229-236.) The speed of quantitation of multiple samples may be accelerated by running the assay in an ELISA format where the oligomer of interest is presented in various dilutions and a spectrophotometric or colorimetric response gives rapid quantitation.

In further embodiments, oligonucleotides or longer fragments derived from any of the polynucleotide sequences described herein may be used as targets in a microarray. The microarray can be used to monitor the expression level of large numbers of genes simultaneously and to identify genetic variants, mutations, and polymorphisms. This information may be used to determine gene function, to understand the genetic basis of a disorder, to diagnose a disorder, and to develop and monitor the activities of therapeutic agents.

Microarrays may be prepared, used, and analyzed using methods known in the art. (See, e.g., Brennan, T.M. et al. (1995) U.S. Patent No. 5,474,796; Schena, M. et al. (1996) Proc. Natl. Acad. Sci. 93:10614-10619; Baldeschweiler et al. (1995) PCT application WO95/251116; Shalon, D. et al. (1995) PCT application WO95/35505; Heller, R.A. et al. (1997) Proc. Natl. Acad. Sci. 94:2150-2155; and Heller, M.J. et al. (1997) U.S. Patent No. 5,605,662.)

In another embodiment of the invention, nucleic acid sequences encoding PHSP may be used to generate hybridization probes useful in mapping the naturally occurring genomic sequence. The sequences may be mapped to a particular chromosome, to a specific region of a chromosome, or to artificial chromosome constructions, e.g., human artificial chromosomes (HACs), yeast artificial chromosomes (YACs), bacterial artificial chromosomes (BACs), bacterial P1 constructions, or single chromosome cDNA libraries. (See, e.g., Harrington, J.J. et al. (1997) Nat Genet. 15:345-355; Price, C.M. (1993) Blood Rev. 7:127-134; and Trask, B.J. (1991) Trends Genet. 7:149-154.)

Fluorescent <u>in situ</u> hybridization (FISH) may be correlated with other physical chromosome mapping techniques and genetic map data. (See, e.g., Heinz-Ulrich, et al. (1995) in Meyers, <u>supra</u>, pp. 965-968.) Examples of genetic map data can be found in various scientific journals or at the Online Mendelian Inheritance in Man (OMIM) site. Correlation between the location of the gene encoding PHSP on a physical chromosomal map and a specific disorder, or a predisposition to a specific disorder, may help define the region of DNA associated with that disorder. The nucleotide sequences of the invention may be used to detect differences in gene sequences among normal, carrier, and affected individuals.

In situ hybridization of chromosomal preparations and physical mapping techniques, such as linkage analysis using established chromosomal markers, may be used for extending genetic maps. Often the placement of a gene on the chromosome of another mammalian species, such as mouse, may reveal associated markers even if the number or arm of a particular human chromosome is not known.

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New sequences can be assigned to chromosomal arms by physical mapping. This provides valuable information to investigators searching for disease genes using positional cloning or other gene discovery techniques. Once the disease or syndrome has been crudely localized by genetic linkage to a particular genomic region, e.g., ataxia-telangiectasia to 11q22-23, any sequences mapping to that area may represent associated or regulatory genes for further investigation. (See, e.g., Gatti, R.A. et al. (1988) Nature 336:577-580.) The nucleotide sequence of the subject invention may also be used to detect differences in the chromosomal location due to translocation, inversion, etc., among normal, carrier, or affected individuals.

In another embodiment of the invention, PHSP, its catalytic or immunogenic fragments, or oligopeptides thereof can be used for screening libraries of compounds in any of a variety of drug screening techniques. The fragment employed in such screening may be free in solution, affixed to a solid support, borne on a cell surface, or located intracellularly. The formation of binding complexes between PHSP and the agent being tested may be measured.

Another technique for drug screening provides for high throughput screening of compounds
15 having suitable binding affinity to the protein of interest. (See, e.g., Geysen, et al. (1984) PCT
application WO84/03564.) In this method, large numbers of different small test compounds are
synthesized on a solid substrate. The test compounds are reacted with PHSP, or fragments thereof,
and washed. Bound PHSP is then detected by methods well known in the art. Purified PHSP can also
be coated directly onto plates for use in the aforementioned drug screening techniques. Alternatively,
20 non-neutralizing antibodies can be used to capture the peptide and immobilize it on a solid support.

In another embodiment, one may use competitive drug screening assays in which neutralizing antibodies capable of binding PHSP specifically compete with a test compound for binding PHSP. In this manner, antibodies can be used to detect the presence of any peptide which shares one or more antigenic determinants with PHSP.

In additional embodiments, the nucleotide sequences which encode PHSP may be used in any molecular biology techniques that have yet to be developed, provided the new techniques rely on properties of nucleotide sequences that are currently known, including, but not limited to, such properties as the triplet genetic code and specific base pair interactions.

Without further elaboration, it is believed that one skilled in the art can, using the preceding description, utilize the present invention to its fullest extent. The following preferred specific embodiments are, therefore, to be construed as merely illustrative, and not limitative of the remainder of the disclosure in any way whatsoever.

The disclosures of all patents, applications, and publications mentioned above and below, in particular U.S. Ser. No. 09/173,482, 09/123,494, 09/152,814, 09/229,005, 60/106,889, 60/109,093, and 60/113,796, are hereby expressly incorporated by reference.

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EXAMPLES

I. Construction of cDNA Libraries

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RNA was purchased from Clontech or isolated from tissues described in Table 4. Some tissues were homogenized and lysed in guanidinium isothiocyanate, while others were homogenized and lysed in phenol or in a suitable mixture of denaturants, such as TRIZOL (Life Technologies), a monophasic solution of phenol and guanidine isothiocyanate. The resulting lysates were centrifuged over CsCl cushions or extracted with chloroform. RNA was precipitated from the lysates with either isopropanol or sodium acetate and ethanol, or by other routine methods.

Phenol extraction and precipitation of RNA were repeated as necessary to increase RNA purity. In some cases, RNA was treated with DNase. For most libraries, poly(A+) RNA was isolated using oligo d(T)-coupled paramagnetic particles (Promega), OLIGOTEX latex particles (OIAGEN, Chatsworth CA), or an OLIGOTEX mRNA purification kit (QIAGEN). Alternatively, RNA was isolated directly from tissue lysates using other RNA isolation kits, e.g., the POLY(A)PURE mRNA 15 purification kit (Ambion, Austin TX).

In some cases, Stratagene was provided with RNA and constructed the corresponding cDNA libraries. Otherwise, cDNA was synthesized and cDNA libraries were constructed with the UNIZAP vector system (Stratagene) or SUPERSCRIPT plasmid system (Life Technologies), using the recommended procedures or similar methods known in the art. (See, e.g., Ausubel, 1997, supra, units 20 5.1-6.6). Reverse transcription was initiated using oligo d(T) or random primers. Synthetic oligonucleotide adapters were ligated to double stranded cDNA, and the cDNA was digested with the appropriate restriction enzyme or enzymes. For most libraries, the cDNA was size-selected (300-1000 bp) using SEPHACRYL S1000, SEPHAROSE CL2B, or SEPHAROSE CL4B column chromatography (Amersham Pharmacia Biotech) or preparative agarose gel electrophoresis. cDNAs 25 were ligated into compatible restriction enzyme sites of the polylinker of a suitable plasmid, e.g., PBLUESCRIPT plasmid (Stratagene), pSPORT1 plasmid (Life Technologies), or pINCY (Incyte Pharmaceuticals, Palo Alto CA). Recombinant plasmids were transformed into competent E. coli cells including XL1-BLUE, XL1-BLUEMRF, or SOLR from Stratagene or DH5α, DH10B, or ELECTROMAX DH10B from Life Technologies.

II. 30 Isolation of cDNA Clones

Plasmids were recovered from host cells by in vivo excision, using the UNIZAP vector system (Stratagene) or cell lysis. Plasmids were purified using at least one of the following: a Magic or WIZARD Minipreps DNA purification system (Promega); an AGTC Miniprep purification kit (Edge Biosystems, Gaithersburg MD); and QIAWELL 8 Plasmid, QIAWELL 8 Plus Plasmid, 35 QIAWELL 8 Ultra Plasmid purification systems or the R.E.A.L. PREP 96 plasmid kit from QIAGEN. Following precipitation, plasmids were resuspended in 0.1 ml of distilled water and stored, with or without lyophilization, at 4°C.

Alternatively, plasmid DNA was amplified from host cell lysates using direct link PCR in a high-throughput format (Rao, V.B. (1994) Anal. Biochem. 216:1-14). Host cell lysis and thermal 5 cycling steps were carried out in a single reaction mixture. Samples were processed and stored in 384-well plates, and the concentration of amplified plasmid DNA was quantified fluorometrically using PICOGREEN dye (Molecular Probes, Eugene OR) and a Fluoroskan II fluorescence scanner (Labsystems Oy, Helsinki, Finland).

III. Sequencing and Analysis

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cDNA sequencing reactions were processed using standard methods or high-throughput instrumentation such as the ABI CATALYST 800 (Perkin-Elmer) thermal cycler or the PTC-200 thermal cycler (MJ Research) in conjunction with the HYDRA microdispenser (Robbins Scientific) or the MICROLAB 2200 (Hamilton) liquid transfer system. cDNA sequencing reactions were prepared using reagents provided by Amersham Pharmacia Biotech or supplied in ABI sequencing kits such as the ABI PRISM BIGDYE Terminator cycle sequencing ready reaction kit (Perkin-Elmer). Electrophoretic separation of cDNA sequencing reactions and detection of labeled polynucleotides were carried out using the MEGABACE 1000 DNA sequencing system (Molecular Dynamics); the ABI PRISM 373 or 377 sequencing systems (Perkin-Elmer) in conjunction with standard ABI protocols and base calling software; or other sequence analysis systems known in the art. Reading 20 frames within the cDNA sequences were identified using standard methods (reviewed in Ausubel, 1997, supra, unit 7.7). Some of the cDNA sequences were selected for extension using the techniques disclosed in Example V.

The polynucleotide sequences derived from cDNA sequencing were assembled and analyzed using a combination of software programs which utilize algorithms well known to those skilled in the art. Table 5 summarizes the tools, programs, and algorithms used and provides applicable descriptions, references, and threshold parameters. The first column of Table 5 shows the tools, programs, and algorithms used, the second column provides brief descriptions thereof, the third column presents appropriate references, all of which are incorporated by reference herein in their entirety, and the fourth column presents, where applicable, the scores, probability values, and other 30 parameters used to evaluate the strength of a match between two sequences (the higher the score, the greater the homology between two sequences). Sequences were analyzed using MACDNASIS PRO software (Hitachi Software Engineering, South San Francisco CA) and LASERGENE software (DNASTAR).

The polynucleotide sequences were validated by removing vector, linker, and polyA sequences and by masking ambiguous bases, using algorithms and programs based on BLAST,

dynamic programing, and dinucleotide nearest neighbor analysis. The sequences were then queried against a selection of public databases, such as the GenBank primate, rodent, mammalian, vertebrate, and eukaryote databases, and BLOCKS to acquire annotation using programs based on BLAST, FASTA, and BLIMPS. The sequences were assembled into full length polynucleotide sequences using programs based on Phred, Phrap, and Consed, and were screened for open reading frames using programs based on GeneMark, BLAST, and FASTA. The full length polynucleotide sequences were translated to derive the corresponding full length amino acid sequences, and these full length sequences were subsequently analyzed by querying against databases such as the GenBank databases (described above), SwissProt, BLOCKS, PRINTS, Prosite, and Hidden Markov Model (HMM)-based protein family databases such as PFAM. HMM is a probabilistic approach which analyzes consensus primary structures of gene families. (See, e.g., Eddy, S.R. (1996) Curr. Opin. Str. Biol. 6:361-365.)

The programs described above for the assembly and analysis of full length polynucleotide and amino acid sequences were also used to identify polynucleotide sequence fragments from SEQ ID NO:32-62. Fragments from about 20 to about 4000 nucleotides which are useful in hybridization and amplification technologies were described in The Invention section above.

IV. Northern Analysis

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Northern analysis is a laboratory technique used to detect the presence of a transcript of a gene and involves the hybridization of a labeled nucleotide sequence to a membrane on which RNAs from a particular cell type or tissue have been bound. (See, e.g., Sambrook, supra, ch. 7; Ausubel, 20 1995, supra, ch. 4 and 16.)

Analogous computer techniques applying BLAST were used to search for identical or related molecules in nucleotide databases such as GenBank or LIFESEQ database (Incyte Pharmaceuticals). This analysis is much faster than multiple membrane-based hybridizations. In addition, the sensitivity of the computer search can be modified to determine whether any particular match is categorized as exact or similar. The basis of the search is the product score, which is defined as:

% sequence identity x % maximum BLAST score

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The product score takes into account both the degree of similarity between two sequences and the length of the sequence match. For example, with a product score of 40, the match will be exact within a 1% to 2% error, and, with a product score of 70, the match will be exact. Similar molecules are usually identified by selecting those which show product scores between 15 and 40, although lower scores may identify related molecules.

The results of northern analyses are reported as a percentage distribution of libraries in which the transcript encoding PHSP occurred. Analysis involved the categorization of cDNA libraries by organ/tissue and disease. The organ/tissue categories included cardiovascular, dermatologic,

developmental, endocrine, gastrointestinal, hematopoietic/immune, musculoskeletal, nervous, reproductive, and urologic. The disease/condition categories included cancer, inflammation/trauma, cell proliferation, neurological, and pooled. For each category, the number of libraries expressing the sequence of interest was counted and divided by the total number of libraries across all categories. Percentage values of tissue-specific and disease- or condition-specific expression are reported in Table 3.

V. **Extension of PHSP Encoding Polynucleotides**

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The full length nucleic acid sequences of SEQ ID NO:32-62 were produced by extension of an appropriate fragment of the full length molecule using oligonucleotide primers designed from this 10 fragment. One primer was synthesized to initiate 5' extension of the known fragment, and the other primer, to initiate 3' extension of the known fragment. The initial primers were designed using OLIGO 4.06 software (National Biosciences), or another appropriate program, to be about 22 to 30 nucleotides in length, to have a GC content of about 50% or more, and to anneal to the target sequence at temperatures of about 68°C to about 72°C. Any stretch of nucleotides which would result in hairpin structures and primer-primer dimerizations was avoided.

Selected human cDNA libraries were used to extend the sequence. If more than one extension was necessary or desired, additional or nested sets of primers were designed.

High fidelity amplification was obtained by PCR using methods well known in the art. PCR was performed in 96-well plates using the PTC-200 thermal cycler (MJ Research, Inc.). The reaction 20 mix contained DNA template, 200 nmol of each primer, reaction buffer containing Mg²⁺, (NH₄)₂SO₄, and β-mercaptoethanol, Taq DNA polymerase (Amersham Pharmacia Biotech), ELONGASE enzyme (Life Technologies), and Pfu DNA polymerase (Stratagene), with the following parameters for primer pair PCI A and PCI B: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 60°C, 1 min; Step 4: 68°C, 2 min; Step 5: Steps 2, 3, and 4 repeated 20 times; Step 6: 68°C, 5 min; Step 7: storage at 4°C. In the alternative, the parameters for primer pair T7 and SK+ were as follows: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 57°C, 1 min; Step 4: 68°C, 2 min; Step 5: Steps 2, 3, and 4 repeated 20 times; Step 6: 68°C, 5 min; Step 7: storage at 4°C.

The concentration of DNA in each well was determined by dispensing 100 µl PICOGREEN quantitation reagent (0.25% (v/v) PICOGREEN; Molecular Probes, Eugene OR) dissolved in 1X TE 30 and 0.5 μl of undiluted PCR product into each well of an opaque fluorimeter plate (Corning Costar, Acton MA), allowing the DNA to bind to the reagent. The plate was scanned in a Fluoroskan II (Labsystems Oy, Helsinki, Finland) to measure the fluorescence of the sample and to quantify the concentration of DNA. A 5 μ l to 10 μ l aliquot of the reaction mixture was analyzed by electrophoresis on a 1 % agarose mini-gel to determine which reactions were successful in extending the sequence.

The extended nucleotides were desalted and concentrated, transferred to 384-well plates, digested with CviJI cholera virus endonuclease (Molecular Biology Research, Madison WI), and sonicated or sheared prior to religation into pUC 18 vector (Amersham Pharmacia Biotech). For shotgun sequencing, the digested nucleotides were separated on low concentration (0.6 to 0.8%) agarose gels, fragments were excised, and agar digested with Agar ACE (Promega). Extended clones were religated using T4 ligase (New England Biolabs, Beverly MA) into pUC 18 vector (Amersham Pharmacia Biotech), treated with Pfu DNA polymerase (Stratagene) to fill-in restriction site overhangs, and transfected into competent <u>E. coli</u> cells. Transformed cells were selected on antibiotic-containing media, individual colonies were picked and cultured overnight at 37°C in 384-well plates in LB/2x carb liquid media.

The cells were lysed, and DNA was amplified by PCR using Taq DNA polymerase (Amersham Pharmacia Biotech) and Pfu DNA polymerase (Stratagene) with the following parameters: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 60°C, 1 min; Step 4: 72°C, 2 min; Step 5: steps 2, 3, and 4 repeated 29 times; Step 6: 72°C, 5 min; Step 7: storage at 4°C. DNA was quantified by PICOGREEN reagent (Molecular Probes) as described above. Samples with low DNA recoveries were reamplified using the same conditions as described above. Samples were diluted with 20% dimethysulphoxide (1:2, v/v), and sequenced using DYENAMIC energy transfer sequencing primers and the DYENAMIC DIRECT kit (Amersham Pharmacia Biotech) or the ABI PRISM BIGDYE Terminator cycle sequencing ready reaction kit (Perkin-Elmer).

In like manner, the nucleotide sequences of SEQ ID NO:32-62 are used to obtain 5' regulatory sequences using the procedure above, oligonucleotides designed for such extension, and an appropriate genomic library.

VI. Labeling and Use of Individual Hybridization Probes

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Hybridization probes derived from SEQ ID NO:32-62 are employed to screen cDNAs, genomic DNAs, or mRNAs. Although the labeling of oligonucleotides, consisting of about 20 base pairs, is specifically described, essentially the same procedure is used with larger nucleotide fragments. Oligonucleotides are designed using state-of-the-art software such as OLIGO 4.06 software (National Biosciences) and labeled by combining 50 pmol of each oligomer, 250 μCi of [γ-³²P] adenosine triphosphate (Amersham Pharmacia Biotech), and T4 polynucleotide kinase (DuPont NEN, Boston MA). The labeled oligonucleotides are substantially purified using a SEPHADEX G-25 superfine size exclusion dextran bead column (Amersham Pharmacia Biotech). An aliquot containing 10⁷ counts per minute of the labeled probe is used in a typical membrane-based hybridization analysis of human genomic DNA digested with one of the following endonucleases: Ase I, Bgl II, Eco RI, Pst I, Xba1, or Pvu II (DuPont NEN).

The DNA from each digest is fractionated on a 0.7% agarose gel and transferred to nylon

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membranes (Nytran Plus, Schleicher & Schuell, Durham NH). Hybridization is carried out for 16 hours at 40°C. To remove nonspecific signals, blots are sequentially washed at room temperature under increasingly stringent conditions up to 0.1 x saline sodium citrate and 0.5% sodium dodecyl sulfate. Hybridization patterns are compared.

VII. Microarrays

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A chemical coupling procedure and an ink jet device can be used to synthesize array elements on the surface of a substrate. (See, e.g., Baldeschweiler, supra.) An array analogous to a dot or slot blot may also be used to arrange and link elements to the surface of a substrate using thermal, UV, chemical, or mechanical bonding procedures. A typical array may be produced by hand 10 or using available methods and machines and contain any appropriate number of elements. After hybridization, nonhybridized probes are removed and a scanner used to determine the levels and patterns of fluorescence. The degree of complementarity and the relative abundance of each probe which hybridizes to an element on the microarray may be assessed through analysis of the scanned images.

Full-length cDNAs, Expressed Sequence Tags (ESTs), or fragments thereof may comprise the elements of the microarray. Fragments suitable for hybridization can be selected using software well known in the art such as LASERGENE software (DNASTAR). Full-length cDNAs, ESTs, or fragments thereof corresponding to one of the nucleotide sequences of the present invention, or selected at random from a cDNA library relevant to the present invention, are arranged on an 20 appropriate substrate, e.g., a glass slide. The cDNA is fixed to the slide using, e.g., UV cross-linking followed by thermal and chemical treatments and subsequent drying. (See, e.g., Schena, M. et al. (1995) Science 270:467-470; Shalon, D. et al. (1996) Genome Res. 6:639-645.) Fluorescent probes are prepared and used for hybridization to the elements on the substrate. The substrate is analyzed by procedures described above.

25 VIII. **Complementary Polynucleotides**

Sequences complementary to the PHSP-encoding sequences, or any parts thereof, are used to detect, decrease, or inhibit expression of naturally occurring PHSP. Although use of oligonucleotides comprising from about 15 to 30 base pairs is described, essentially the same procedure is used with smaller or with larger sequence fragments. Appropriate oligonucleotides are 30 designed using OLIGO 4.06 software (National Biosciences) and the coding sequence of PHSP. To inhibit transcription, a complementary oligonucleotide is designed from the most unique 5' sequence and used to prevent promoter binding to the coding sequence. To inhibit translation, a complementary oligonucleotide is designed to prevent ribosomal binding to the PHSP-encoding transcript.

IX. Expression of PHSP

Expression and purification of PHSP is achieved using bacterial or virus-based expression 35

systems. For expression of PHSP in bacteria, cDNA is subcloned into an appropriate vector containing an antibiotic resistance gene and an inducible promoter that directs high levels of cDNA transcription. Examples of such promoters include, but are not limited to, the trp-lac (tac) hybrid promoter and the T5 or T7 bacteriophage promoter in conjunction with the lac operator regulatory element. Recombinant vectors are transformed into suitable bacterial hosts, e.g., BL21(DE3). Antibiotic resistant bacteria express PHSP upon induction with isopropyl beta-Dthiogalactopyranoside (IPTG). Expression of PHSP in eukaryotic cells is achieved by infecting insect or mammalian cell lines with recombinant Autographica californica nuclear polyhedrosis virus (AcMNPV), commonly known as baculovirus. The nonessential polyhedrin gene of baculovirus is replaced with cDNA encoding PHSP by either homologous recombination or bacterial-mediated transposition involving transfer plasmid intermediates. Viral infectivity is maintained and the strong polyhedrin promoter drives high levels of cDNA transcription. Recombinant baculovirus is used to infect Spodoptera frugiperda (Sf9) insect cells in most cases, or human hepatocytes, in some cases. Infection of the latter requires additional genetic modifications to baculovirus. (See Engelhard, E. K. 15 et al. (1994) Proc. Natl. Acad. Sci. USA 91:3224-3227; Sandig, V. et al. (1996) Hum. Gene Ther. 7:1937-1945.)

In most expression systems, PHSP is synthesized as a fusion protein with, e.g., glutathione S-transferase (GST) or a peptide epitope tag, such as FLAG or 6-His, permitting rapid, single-step, affinity-based purification of recombinant fusion protein from crude cell lysates. GST, a 26-20 kilodalton enzyme from Schistosoma japonicum, enables the purification of fusion proteins on immobilized glutathione under conditions that maintain protein activity and antigenicity (Amersham Pharmacia Biotech). Following purification, the GST moiety can be proteolytically cleaved from PHSP at specifically engineered sites. FLAG, an 8-amino acid peptide, enables immunoaffinity purification using commercially available monoclonal and polyclonal anti-FLAG antibodies (Eastman Kodak). 6-His, a stretch of six consecutive histidine residues, enables purification on metal-chelate resins (QIAGEN). Methods for protein expression and purification are discussed in Ausubel (1995, supra, ch 10 and 16). Purified PHSP obtained by these methods can be used directly in the following activity assay.

X. Demonstration of PHSP Activity

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PHSP protein kinase is measured by the phosphorylation of a substrate in the presence of gamma-labeled ³²P-ATP. PHSP is incubated with an appropriate substrate and ³²P-ATP in a buffered solution. ³²P-labeled product is separated from free ³²P-ATP by gel electrophoresis or chromatographic procedures, and the incorporated ³²P is quantified by phosphorimage analysis or using a scintillation counter. The amount of ³²P detected is proportional to the activity of PHSP in this assay. The specific amino acid residue phosphorylated by PHSP may be determined by

phosphoamino acid analysis of the labeled, hydrolyzed protein.

PHSP phosphatase activity is measured by the removal of phosphate from a [32P]-labelled substrate. PHSP is incubated with an appropriate [32P]-labelled substrate in a buffered solution. Reaction products are separated by gel electrophoresis or chromatographic procedures, and the level of 32P associated with the substrate molecule is quantified by phospho-image analysis or scintillation counting. The difference in 32P associated with untreated substrate versus PHSP-treated substrate is a measure of phosphatase activity and is proportional to PHSP activity.

XI. Functional Assays

PHSP function is assessed by expressing the sequences encoding PHSP at physiologically elevated levels in mammalian cell culture systems. cDNA is subcloned into a mammalian expression vector containing a strong promoter that drives high levels of cDNA expression. Vectors of choice include pCMV SPORT (Life Technologies) and pCR3.1 (Invitrogen, Carlsbad CA), both of which contain the cytomegalovirus promoter. $5-10~\mu\mathrm{g}$ of recombinant vector are transiently transfected into a human cell line, preferably of endothelial or hematopoietic origin, using either liposome 15 formulations or electroporation. 1-2 μ g of an additional plasmid containing sequences encoding a marker protein are co-transfected. Expression of a marker protein provides a means to distinguish transfected cells from nontransfected cells and is a reliable predictor of cDNA expression from the recombinant vector. Marker proteins of choice include, e.g., Green Fluorescent Protein (GFP; Clontech), CD64, or a CD64-GFP fusion protein. Flow cytometry (FCM), an automated, laser optics-20 based technique, is used to identify transfected cells expressing GFP or CD64-GFP and to evaluate properties, for example, their apoptotic state. FCM detects and quantifies the uptake of fluorescent molecules that diagnose events preceding or coincident with cell death. These events include changes in nuclear DNA content as measured by staining of DNA with propidium iodide; changes in cell size and granularity as measured by forward light scatter and 90 degree side light scatter; down-regulation of DNA synthesis as measured by decrease in bromodeoxyuridine uptake; alterations in expression of cell surface and intracellular proteins as measured by reactivity with specific antibodies; and alterations in plasma membrane composition as measured by the binding of fluorescein-conjugated Annexin V protein to the cell surface. Methods in flow cytometry are discussed in Ormerod, M. G. (1994) Flow Cytometry, Oxford, New York NY.

The influence of PHSP on gene expression can be assessed using highly purified populations of cells transfected with sequences encoding PHSP and either CD64 or CD64-GFP. CD64 and CD64-GFP are expressed on the surface of transfected cells and bind to conserved regions of human immunoglobulin G (IgG). Transfected cells are efficiently separated from nontransfected cells using magnetic beads coated with either human IgG or antibody against CD64 (DYNAL, Lake Success NY). mRNA can be purified from the cells using methods well known by those of skill in the art.

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Expression of mRNA encoding PHSP and other genes of interest can be analyzed by northern analysis or microarray techniques.

XII. Production of PHSP Specific Antibodies

PHSP substantially purified using polyacrylamide gel electrophoresis (PAGE; see, e.g., Harrington, M.G. (1990) Methods Enzymol. 182:488-495), or other purification techniques, is used to immunize rabbits and to produce antibodies using standard protocols.

Alternatively, the PHSP amino acid sequence is analyzed using LASERGENE software (DNASTAR) to determine regions of high immunogenicity, and a corresponding oligopeptide is synthesized and used to raise antibodies by means known to those of skill in the art. Methods for selection of appropriate epitopes, such as those near the C-terminus or in hydrophilic regions are well described in the art. (See, e.g., Ausubel, 1995, supra, ch. 11.)

Typically, oligopeptides 15 residues in length are synthesized using an ABI 431A peptide synthesizer (Perkin-Elmer) using fmoc-chemistry and coupled to KLH (Sigma-Aldrich, St. Louis MO) by reaction with N-maleimidobenzoyl-N-hydroxysuccinimide ester (MBS) to increase immunogenicity. (See, e.g., Ausubel, 1995, supra.) Rabbits are immunized with the oligopeptide-KLH complex in complete Freund's adjuvant. Resulting antisera are tested for antipeptide activity by, for example, binding the peptide to plastic, blocking with 1% BSA, reacting with rabbit antisera, washing, and reacting with radio-iodinated goat anti-rabbit IgG.

XIII. Purification of Naturally Occurring PHSP Using Specific Antibodies

Naturally occurring or recombinant PHSP is substantially purified by immunoaffinity chromatography using antibodies specific for PHSP. An immunoaffinity column is constructed by covalently coupling anti-PHSP antibody to an activated chromatographic resin, such as CNBr-activated SEPHAROSE (Amersham Pharmacia Biotech). After the coupling, the resin is blocked and washed according to the manufacturer's instructions.

Media containing PHSP are passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of PHSP (e.g., high ionic strength buffers in the presence of detergent). The column is eluted under conditions that disrupt antibody/PHSP binding (e.g., a buffer of pH 2 to pH 3, or a high concentration of a chaotrope, such as urea or thiocyanate ion), and PHSP is collected.

30 XIV. Identification of Molecules Which Interact with PHSP

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PHSP, or biologically active fragments thereof, are labeled with ¹²⁵I Bolton-Hunter reagent. (See, e.g., Bolton et al. (1973) Biochem. J. 133:529.) Candidate molecules previously arrayed in the wells of a multi-well plate are incubated with the labeled PHSP, washed, and any wells with labeled PHSP complex are assayed. Data obtained using different concentrations of PHSP are used to calculate values for the number, affinity, and association of PHSP with the candidate molecules.

Various modifications and variations of the described methods and systems of the invention will be apparent to those skilled in the art without departing from the scope and spirit of the invention. Although the invention has been described in connection with specific preferred embodiments, it should be understood that the invention as claimed should not be unduly limited to such specific embodiments. Indeed, various modifications of the described modes for carrying out the invention which are obvious to those skilled in molecular biology or related fields are intended to be within the scope of the following claims.

TABLE

Protein SEQ ID NO:	Nucleotide SEQ ID NO:	Clone ID	Library	Fragments
1	32	132240	BMARNOT02	132240H1 and 132240R1 (BMARNOT02), 3254142H1 (OVARTUN01), 1453821X14F1 and 1453821F6 (PENITUT01)
2	33	2180116	SININOT01	2180116H1 and 2180116T6 (SININOT01), 3046645H1 (HEAANOT01), 1918183H1 (PROSNOT06), and 1482405F1 (CORPNOT02)
3	34	2197671	SPLNFET02	2197671H1 (SPLNFET02), 666366X22R1 (SCORNOT01), 693783X14 (SYNORAT03), 824265X33F1 (PROSNOT06), 039482R1 and 039482F1 (HUVENOB01), 1453984T6 (PENITUT01), 1663987H1 (BRSTNOT09), and 125901R1 (LUNGNOT01)
4	35	2594943	OVARTUT02	2594943H1 (OVARTUT02), 3617557H1 (EPIPNOT01), 2269005R6 (UTRSNOT02), 1307764F6 (COLNFET02), 1377794F6 (LUNGNOT10), and 1286608H1 (BRAINOT11)
5	36	1513871	PANCTUT01	754239R6 (BRAITUT02), 1513871H1 (PANCTUT01), 2414420F6 (HNT3AZT01), 3291775F6 (BONRFET01), 3821451F6 (BONSTUT01)
9	37	156108	тнр1Рьв02	156108F1 and 156108H1 (THP1PLB02), 336346R6 (EOSIHET02), 1319528F1 (BLADNOT04), 2375549F6 (ISLTNOT01), SBFA04563F1, SBFA04977F1
7	38	2883243	UTRSTUT05	1342082F6 (COLNTUT03), 1933387T6 (COLNNOT16), 2766460F6 (BRSTNOT12), 2883243H1 (UTRSTUT05), 3524262H1 (ESOGTUN01), 3766487F6 (BRSTNOT24)

Protein SEQ ID NO:	Nucleotide SEQ ID NO:	Clone ID	Library	Fragments
ω.	39	3173355	UTRSTUT04	1300803F6 and 1300803T6 (BRSTNOT07), 2477542F6 (SMCANOT01), 2477542T6 (SMCANOT01), 2875968H1 (THYRNOT10), 3173355F6 and 3173355H1 (UTRSTUT04), 3290825H1 (BONRFET01), 5192561H1 (OVARDIT06)
6	40	5116906	SMCBUNT01	267517F1 (HNT2NOT01), 263823R1 (HNT2AGT01), 5116906H1 (SMCBUNT01)
10	41	940589	ADRENOT03	029801R6 (SPLNFET01), 940589H1 (ADRENOT03), 1737403T6 (COLNNOT22), 1805477F6 and 1805477T6 (SINTNOT13), 2447613H1 (THP1NOT03), 3408563H1 (PROSTUS08), 3519506H1 (LUNGNON03), 3637343T6 (LUNGNOT30)
11	42	304421	TESTNOT04	304421H1, 304421X318B2, and 304421X323B2 (TESTNOT04), 2639579F6 (BONTNOT01), 2951859H1 (KIDNFET01)
12	43	1213802	BRSTTUT01	894574R1 (BRSTNOT05), 1213802H1 (BRSTTUT01), 1233414F1 and 1234238H1 (LUNGFET03), 1255782F2 and 1255782T1 (MENITUT03), 1455429F1 (COLNFET02), 1576102T1 (LNODNOT03), 2189267F6 (PROSNOT26), 2748179F6 (LUNGTUT11), 2831667H1 (TLYMNOT03), 3031229H1 (TLYMNOT05), 3054893H1 (LNODNOT08), 3797030F6 (SPLNNOT12), 3880154H1 (SPLNNOT11), 4852525H1 (TESTNOT10), 5514137H1 (BRADDIR01), 5518378H1
13	44	1378134	LUNGNOT10	1378134H1 and 1378134X11 (LUNGNOT10), 2205185F6 (SPLNFET02), 4959694H1 (TLYMNOT05), SAMA00107F1, SAMA00160F1, SAMA00020F1

Protein	Nucleotide	Clone ID	Library	Fragments
SEQ ID NO:	SEQ ID NO:			
14	45	1490070	UCMCL5T01	432218H1 (BRAVUNT02), 1490070H1 (UCMCL5T01), 1535394F1 (SPLNNOT04), 1616509F6 and 1616509T6 (BRAITUT12), 2490845H1 (EOSITXT01), 2723789F6 (LUNGTUT10), SAOA00263F1
15	46	1997814	BRSTTUT03	855350R1 (NGANNOT01), 875417R1 (LUNGAST01), 895096R1 (BRSTNOT05), 1271348F1 (TESTTUT02), 1331289F6 (PANCNOT07), 1359243F1 (LUNGNOT12), 1540824T1 (SINTTUT01), 1839828H1 (EOSITXT01), 1997814H1 (BRSTTUT03), 2170638F6 (ENDCNOT03), 3751363F6 (UTRSNOT18)
16	47	2299715	BRSTNOT05	637354R6 and 637354T6 (NEUTGMT01), 1852144F6 (LUNGFET03), 2172576F6 (ENDCNOT03), 2232449F6 (PROSNOT16), 2299715H1 (BRSTNOT05), 2509737X325D2 (CONUTUT01), 2606210F6 (LUNGTUT07), 2692024F6 (LUNGNOT23), 2805893F6 (BLADTUT08), 2986160H1 (CARGDIT01), 3085382H1 (HEAONOT03), 3136101F6 and 3136587H1 (SMCCNOT01), 4249977H1 (BRADDIR01)
17	48	209854	SPLNNOT02	209854H1 and 209854T6 (SPLNNOT02), 3152165R6 and 3152165T6 (ADRENON04)
18	49	1384286	BRAITUT08	676123R6 and 676123T6 (CRBLNOT01), 989218X11 and 989218X12 (LVENNOT03), 1384286H1 (BRAITUT08), 3099868H1 (PROSBPT03), 4693167H1 (BRAENOT02)
19	50	1512656	PANCTUT01	322847X5 (EOSIHET02), 1253795T6 (LUNGFET03), 1512656H1 (PANCTUT01), 1561686X303D1 (SPLNNOT04), 2212305H1 (SINTFET03), 2697679H1 (UTRSNOT12), 3205172H1 (PENCNOT03), 5313318H1 (KIDETXS02)

	Nucleotide	Clone ID	Library	Fragments
SEQ ID NO:	SEQ ID NO:			
20	51	2098635	BRAITUT02	1268848T1, 1268848X301F1, and 2157157H1 (BRAINOT09), 2098635H1 and 2098635R6 (BRAITUT02), 2198819F6, 2198819X301D4, 2198819X303D1, 2198819X309B2, and 2198819X309D4 (SPLNFET02), 2784975H2 (BRSTNOT13), 3320340H1 (PROSBPT03)
21	52	2446646	THP1NOT03	000297R6 and 000297X61 (U937NOT01), 2446646H1 (THP1NOT03), 2557274F6 (THYMNOT03)
22	53	2764911	BRSTNOT12	678618T6 and 678618X14 (UTRSNOT02), 2304126R6 (BRSTNOT05), 2764911H1 (BRSTNOT12), 2834475F6 (TLYMNOT03), 2915803F6 (THYMFET03), 3035012F6 (TLYMNOT05), SAFC00027F1, SAFC00254F1, SAFC02376F1, SAFC01609F1
23	54	3013946	MUSCNOT07	673753H1 (CRBLNOT01), 989218X11 and 989218X14 (LVENNOT03), 2821720F6 (ADRETUT06), 3013946F6, 3013946H1, and 3013946T6 (MUSCNOT07), 4693167H1 (BRAENOT02)
24	55	196190	HUVESTB01	067967X92, 067966R1, and 067967H1 (HUVESTB01), SAIA02074F1, SAIA03254F1, SAIA03603F1, and SAIA02259F1
25	56	346275	THYMNOT02	346275H1 (THYMNOT02), 609792X12 (COLAMOT01), SAGA03543F1, SAGA02528F1, and SAGA00285F1
26	57	283746	CARDNOT01	283746H1 and 283746X10 (CARDNOT01), 4903108H1 (TLYMNOT08), 557918X15 (MPHGLPT02), and 2379045F6 (ISLTNOT01)
27	58	2696537	UTRSNOT12	2696537H1 (UTRSNOT12), 3173337F6 (UTRSTUT04), 082658X100 (HUVESTB01), and 603219T6 (BRSTTUT01)

Protein SEQ ID NO:	Protein Nucleotide SEQ ID NO: SEQ ID NO:	Clone ID Library	Library	Fragments
28	95	551178	BEPINOT01	551178H1 (BEPINOT01), 861522R1 (BRAITUT03), 965838R1 (BRSTNOT05), 1574007F1 and 1574007T1 (LNODNOT03), 1830083T6 and 1831194T6 (THP1AZT01), 3098496H1 (CERVNOT03), 3293481H1 (TLYJINT01)
29	09	619292	PGANNOT01	613165F1 (COLNTUT02), 619292H1 and 619292X13 (PGANNOT01)
30	61	2054049	BEPINOT01	1736355F6 (COLNNOT22), 2054049H1 (BEPINOT01), 2379092T6 (ISLTNOT01), 3127284T3 (LUNGTUT12), 3136377F6 (SMCCNOT01), SBMA00545F1, SBMA00827F1, SBMA02930F1, SBMA02853F1
31	62	2843910	DRGLNOT01	036294X71 (HUVENOB01), 066017X102, 068399R1, and 068399X3 (HUVESTB01), 1527276H1 (UCMCL5T01), 1846570T6 (COLNNOT09), 2843910H1 (DRGLNOT01)

ABLE 2

Polypeptide	Amino	Potential	Potential	Signature Sequence	Homologous	Analytical
SEQ ID NO:	Acid Residues	Phosphorylation Glycosylation Sites	Glycosylation Sites		sednences	Methods
г	300	S3 S15 S19 S20 S24 T98 S125 S231 T238 S257 S282 S12 S41 S70 T120 T143 S146 T242	N85 N88 N96	Protein kinase motifs: G161-F256 catalytic tk domain IX: V180-E202	Protein kinase	BLAST PFAM PRINTS
2	147	S85 T38 S90		Calcium-binding repeat motifs: G28-L115	PKC- potentiated inhibitory protein of PP1 (CP117)	BLAST PRINTS BLOCKS
m	431	T178 S282 T25 S34 S75 S106 S194 S198 T208 T264 S299 S303 S304 S308 T328 S345 S388 T46 S137 S260	N44 N242	PTK signatures: A18-Y283 ATP-binding site: I30-K53, E127-G164 Y196-H219 PK catalytic subdomains: M99-E112, Y134-L152 G181-I191, Y243-	Ste20-like protein kinase	BLOCKS PRINTS PROFILESCAN BLAST
4	218	S108 S68 S90 T133 T170 S172 T34 T123 T207		Phosphofructokinase domains: I47, V177-Q195 L148-Y164		PRINTS

Polypeptide SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequence	Homologous sequences	Analytical Methods
ហ	474	S14 S89 S98 S132 S472 T22 S26 S62 S66 T204 T320 T345 T359 S427 S443 S94 S128 T211 T336 S443 Y155		Protein kinase family signature: Y144-F425	serine /threonine protein kinase	MOTIFS PFAM BLOCKS PRINTS ProfileScan BLAST
9	540	S102 S183 S267 T296 T301 S442 S34 S58 S180 S207 S224 T360 S374 S401 S428 S478 T484 Y23	N100 N391 N457 N537	Protein kinase family signature: L18-L287	serine /threonine protein kinase	MOTIFS PFAM BLOCKS PRINTS PROFILESCAN BLAST
٢	454	S57 S69 S130 T203 T212 S338 S420 S91 T101 T220 S271 S295 T315 S359 S381 Y197	N55 N140 N218 N403 N437 N441	SH2 domain: W63-Y138, W354-Y428 PI 3 kinase P85 regulator: K153-G176, A216- N257, R287-N332	phosphatidyl- inositol 3- kinase	PFAM BLOCKS PRINTS BLAST
ω	502	S246 T498 T21 S65 S76 T193 T203 S275 S312 S355 T484 S106 T222 S323 T498 Y347	N302 N414	Signal petide: M1-T21 SH2 domain: V70-E80 ER targeting signal: K499-L502	tyrosine kinase	SigPept BLOCKS MOTIFS BLAST

Polypeptide SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequence	Homologous sequences	Analytical Methods
o.	281	T66 T140 T141 T182 S210	N117 N139	Signal peptide: M1-176	calcium /calmodulin- dependent protein kinase	PFAM BLAST
10	510	T297 S323 S358 S51 T312 S323 T325 S329 T377 T390 T483 S24 S152 T201 S210 S247 T292 T406	N185 N349 N381 N405	Protein kinase family signature: R52-V261	Serine /threonine protein kinase	PFAM BLOCKS PRINTS MOTIFS BLAST
11	248	S5 S20 S36 T210 T245	N208	Tyrosine specific phosphatase active site: F166-A220 Dual specificity phosphatase: H95-R240	Tyrosine phosphatase or Dual specificity phosphatase	BLAST, MOTIFS BLOCKS, PRINTS PROFILESCAN PFAM

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Polypeptide	Amino	Potential	Potential	Signature Sequence	Homologous	Analytical
SEQ ID NO:	Acid Residues	Phosphorylation Sites	Glycosylation Sites		sednences	Methods
12	810	S62 S290 T429 S758 T17 T104 S108 T216 S279 T316 S330 T360 S386 T405 S425 S465 T473 S497 T547 T561 T715 S733 S738 S768 S196 S222 S229 S267 T281 T321 T347 S370 T400 T512 S534 T609 S617 S663 S751	N 3 3		Protein kinase	BLAST, MOTIFS
13	549	S6 T502 T21 T116 S125 S320 T417 S46 S87 T240 S390 S397 S405 S430 S497	N238	ATP/GTP-binding site (p-loop): G58-T65 Protein kinase signature: I176-K199 I292-L304 Y347-L370 F456-L483	Dual specificity tyrosine /serine protein kinase	BLAST, MOTIFS BLOCKS, PRINTS PFAM
14	416	S312 T20 T97 S104 S183 T185 T211 T274 S381 S411 S72 S79 S140 S318 Y53		SH3 domain: A366-D384 N402-E414	PEST phosphatase interacting protein	BLAST, MOTIFS BLOCKS, PRINTS PFAM

Polypeptide SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequence	Homologous sequences	Analytical Methods
15	425	T34 S233 S234 S25 S107 T144 T198 T250 S251 S258 S282 S300 S324 S345 T390 T51 T133 S365 S383 Y71	N23 N176 N362		SH3 binding protein	BLAST, MOTIFS
16	1135	S54 S815 S9 S17 T59 S112 T124 T222 S264 T319 S324 S326 S50 T572 S625 S681 S682 T688 T689 S706 S720 T931 S958 S978 S999 S255 T309 T351 T543 S550 S624 S632 S726 T811 S898 S1012 S1113 Y321 Y323	N33 N570 N718	Protein kinase signature: V31-K54 V149-L161 W129-V182 Tyrosine kinase catalytic site: G190-1200 S214-M236 NIK1-like kinase domain: Y836-R1115	NIK kinase	BLAST, MOTIFS PROFILESCAN BLOCKS, PRINTS PFAM
17	228	T163 S60 T78 T68 S88 S147	N19 N100 N114		Interferon- induced PK regulator (P52rIPK)	BLAST

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Polypeptide SEQ ID NO:	Amino Acid Residues	Potential Potential Phosphorylation Glycosylation Sites	Potential Glycosylation Sites	Signature Sequence	Homologous sequences	Analytical Methods
18	503	S51 T262 T36 S79 T94 S109 T361 T362 T403 S472 T47 S334 S343 Y17	N313 N333 N360	Protein kinase signature: I20-K43 V132-L144 V195-E217 Protein kinase domain: Y14-V272	calcium /calmodulin- dependent protein kinase II, beta 3 isoform	BLAST, BLOCKS, PRINTS, MOTIFS, PFAM, PROFILESCAN
19	433	S12 S77 S124 S131 S255 S290 T327 S365 S402 T70 Y88			Choline kinase isolog 384D8_3	BLAST, MOTIFS
20	527	S417 S154 S199 T367 S453 T120 S178 S413 T447 S473	N470	Protein kinase signature: 1144-K167 1260-V172 ATP-binding site: Q247-G284 Y318-F341 Protein kinase domain: 1138-L427	MAP-related protein kinase	BLAST, BLOCKS MOTIFS, PFAM, PROFILESCAN

Polypepride							
Residues Sites Sites Recidues Sites Recidues Sites Signature: Protein Kinase Protein Rinase	Polypeptide SEQ ID NO:	Amino Acid			Signature Sequence	Homologous sequences	Analytical Methods
322 S19 S122 T198 N196 N249 Protein kinase Protein PROPTIES, 1260 S264 T301 L163-L175 Kinase PROPTIES, 1260 S264 T301 ATP-binding site: H150-H207 M150-V187 M150-V187 M150-V187 M150-V187 M150-V187 M150-V187 M150-V187 M150-V187 M150-V187 M150-M187 M150		Residues	Sites	Sites			
T200 T236 S251 Signature:	21	322	122 1	N196 N249	Protein kinase	Protein	
T260 \$264 T301			T236		signature:	tyrosine	
S14 552 T181			S 264		L163-I175	kinase	
M150-V187 Protein kinase domain: S12-H24 Protein kinase domain: S12-H24 Protein kinase domain: S12-H24 Protein kinase domain: T14 T98 S144 L55-K81, L432-K455 Protein kinase PRINTS, L55-K81, L432-K455 Protein kinase PRINTS, L750 S13 T751 PROFILE E16-G197, H212-R255 PROFILE E16-G197, H21			S14 S52 T181				PROFILESCAN
Rocean State Ribosomal Science			T225		M150-V187		
Rocean Ribosomal S6 BLAST, S12-E316 S12-E316 S12-E316 S12-E316 S144 S144 S144 S144 S144 S144 S1455 L55-K81, L432-K455 Protein kinase PRINTS, L55-K81, L432-K455 PROFILE E160-G197, H232-E255 S758 T27 T74 H534-F552, C603-H625 S758 T27 T74 H534-F552, C603-H625 PROFILE E160-G197, H232-E255 PROFILE E160-G197, H232					I224-H247		
802 \$70 T87 \$550 N36 N655 Protein kinase Ribosomal \$6 BLAST, 1150 \$230 \$253 T14 T98 \$144 Protein kinase Pro					Protein kinase domain:		
802 \$70 T87 \$750 \$186 M36 M655 \$19 Protein kinase \$114 T98 \$144 \$144 T98 \$144 \$145 S230 \$263 \$145 T150 \$230 \$263 \$146 T150 \$230 \$263 \$146 T150 \$230 \$263 \$146 T470 \$145 T470 \$160 T207 \$268 \$160 T207 \$268 \$268 \$268 \$268 \$268 \$268 \$268 \$268					S32-E316		
T14 T98 S144 signature: signature: protein kinase PRINTS, T150 S230 S263	22	802	T87 S	N36 N655	Protein kinase	Ribosomal S6	
T150 S230 S263 T150 S230 S263 T150 T263 T465 T470 T100 T207 S268 T100 T207 S268 T100 T207 S268 T100 T207 S268 T27 T74 T100 T207 S268 T27 T74 T262 S398 T27 T74 T27 T262 S398 T27			T98 S		signature:	protein kinase	
## PROFILE PROFILE S517 S633 T465 T470			\$230		L55-K81, L432-K455		
S517 S633 T751 S158 T27 T74 T100 T207 S268 S368 S458 S368 S458 F49-F318, L427-L687 Protein kinase C domain: 641 S51 T262 S398 N313 N332 Frotein kinase Ca2+ Gomain: A175 T376 T541 S610 T47 S315 S333 S342 S393 S474 S508 Y17 Y14-V272 S758 T27 T74 FT60-G197, H232-F255 FT78 Catalytic domain: F49-F318, L427-L687 Protein kinase C domain: Q319-I382 Q319-I382 Ca2+ A24-F552, C603-H625 Protein kinase C domain: Q319-I382 Ca2+ MOTIFS, MOTIFS, Y191-F214 Protein kinase domain: Y191-F214 Protein kinase domain: Y14-V272			T465		ATP-binding site:		PROFILESCAN
## ST58 T27 T74 PTK catalytic domain: T100 T207 S268 S458 Protein kinase domains: F49-F318, L427-L687 Protein kinase C domain: Q319-I382 Protein kinase C dependent HOTIES, T375 T376 T541 S610 T47 S315 V132-L144 PRINTS, T375 T376 T541 ATP-binding site: Q119-A156 S422 S431 S465 Protein kinase domain: S474 S508 Y17 Y14-V272 Y14-V272			S633		E160-G197, H232-F255		
T100 T207 S268 S368 S458 S368 S458 Protein kinase domains: F49-F318, L427-L687 Protein kinase C domain: Q319-I382 S436 S479 T36 S79 T94 S109 T375 T376 T541 S610 T47 S315 S333 S342 S393 S474 S508 Y17 Y14-V272			T27		PTK catalytic domain:		
S368 S458 Protein kinase domains: F49-F318, L427-L687			T207	_	H534-F552, C603-H625		
641 S51 T262 S398 N313 N32 Protein kinase C domain:			œ		Protein kinase domains:		
641 S51 T262 S398 N313 N332 Protein kinase C 641 S51 F262 S398 N313 N332 Protein kinase S79 T94 S109 T375 T376 T541 S610 T47 S315 S333 S342 S393 S474 S508 Y17 Y14-V272 Frotein kinase C domain: O319-I382 Ca2+ BLAST, ACAImodulin PRINTS, dependent MOTIFS, ATP-binding site: O119-A156 Y191-F214 Protein kinase domain: Y14-V272					F49-F318, L427-L687		
641 S51 T262 S398 N313 N332 Protein kinase Ca2+ BLAST, Academin S436 S479 T36 N374 Signature: Signature: Academin /calmodulin PRINTS, Academin T375 T376 T541 V132-L144 protein kinase PROFILE S610 T47 S315 ATP-binding site: Q119-A156 protein kinase PROFILE S432 S431 S465 Protein kinase domain: Y14-V272 Y14-V272					Protein kinase C		
641 S51 T262 S398 N313 N332 Protein kinase Ca2+ S436 S479 T36 N374 Signature: S79 T94 S109 T375 T376 T541 S610 T47 S315 S333 S342 S393 S422 S431 S465 S474 S508 Y17 Y14-V272					domain:		
641 S51 T262 S398 N313 N332 Protein kinase Ca2+ S436 S479 T36 S79 T94 S109 T375 T376 T541 S610 T47 S315 S333 S342 S393 S422 S431 S465 S474 S508 Y17 Y14-V272 S436 S479 T36 S437 S465 S438 S474 S508 Y17 Y14-V272 S436 S478 S398 S474 S508 Y17 Y14-V272					Q319-I382		
S479 T36 N374 signature: /calmodulin 94 S109 120-K43 dependent T376 T541 V132-L144 protein kinase T47 S315 ATP-binding site: Q119-A156 S342 S393 V191-F214 S508 Y17 Protein kinase domain: Y14-V272 Y14-V272	23	641	l	1	Protein kinase	Ca2+	
94 S109 120-K43 dependent T376 T541 V132-L144 protein kinase T47 S315 ATP-binding site: Q119-A156 S342 S393 Q119-A156 Y191-F214 S508 Y17 Protein kinase domain: Y14-V272			S479	N374	signature:	/calmodulin	PRINTS,
T376 T541 V132-L144 protein kinase T47 S315 ATP-binding site: Q119-A156 S431 S465 Y17 Protein kinase domain: Y14-V272			S79 T94 S109		I20-K43	dependent	MOTIFS, PFAM,
T47 S315 S342 S393 S431 S465 S508 Y17			T376		V132-L144	protein kinase	PROFILESCAN
S342 S393 S431 S465 S508 Y17			T47				
S431 S465 S508 Y17			5342		Q119-A156		
S508 Y17			5431		Y191-F214		
Y14-V272			\$508		Protein kinase domain:		
					Y14-V272		

Polypeptide SEQ ID NO:	Amino Acid Residues	Potential Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequence	Homologous sequences	Analytical Methods
24	288	S106 T155 S359 T388 T456 T531 T4, S58 S108 T126 S132 T279 S350 S436 S469 S508 S537 Y32	N63 N130 N574	Protein kinase catalytic domain: Y209-S445, F495-I522 ATP-binding site: I215-K238 STK core catalytic motif: I331-L343	Protein kinase Dyrk2	MOTIFS PFAM BLOCKS PRINTS BLAST
25	389	S31 T301 S56 S96 S134 T149 S186 S201 S283 S358 S375 Y148 Y165	N257 N343 N364	Protein kinase catalytic domain: E73-1311 STK core catalytic motif: 1172-Y184 PTK core domain: D152-D208	CaM-like protein kinase	BLAST PFAM MOTIFS BLOCKS PRINTS PROFILESCAN
26	343	S68 S81 S137 S184 T219 S276 S297 T29 T125 Y86 Y211	N332	EF hand calcium-binding signature: D176-L188	protein phosphatase 2A (PR72)	BLAST MOTIFS BLOCKS
27	184	S36 T105 S40 S70 T117 Y50	N62	Tyrosine phosphatase active site domain: L63-V118	MAP kinase phosphatase (X17C)	BLAST PROFILESCAN BLOCKS PRINTS MOTIFS

Polypeptide	Amino	Potential	Potential	Signature Sequence	Homologous	Analytical
SEQ ID NO:	Acid Residues	Phosphorylation Sites	Glycosylation Sites		sednences	Methods
28	367	S10 S21 S44 S103 T116 T267 T309 S191 S213	N16 N17		protein phosphatase 2A, A-subunit	BLAST
		S218 S256 T305 S352 Y159 Y344				
29	118	S34 S84	N43	Signal peptide: M1-A27	tyrosine phosphatase	SPScan PFAM
				PDZ domain: H8-S73		BLAST
30	356	S9 S94 T209	N333	tyrosine-specific	tyrosine	PROFILESCAN
		T220 S259 S337 S5 S26 S75 S121		protein phosphatase	phosphatase (myotubularin)	MOTIFS
		T154 S282 S332		1108-K164		PRINTS
		S339 Y15 Y84				BLAST
31	453	_	N43 N67 N357	protein phosphatase 2A	protein	PFAM
		S131 S193 S200 T236 S293 S341		p55 subunit: p10-x451	phosphatase 2A	MOTIFS
					subunit, alpha	PRINTS
		T214 S252 T256			isoform	BLAST
	-	S282 S302 S313				
	,	S391 S397				

TABLE 3

Nucleotide SEQ ID NO:	Tissue Expression (Fraction of Total)	Disease or Condition (Fraction of Total)	Vector
32	<pre>Hematopoietic/Immune (0.333) Reproductive (0.333)</pre>	Cell proliferation (0.500) Inflammation (0.333)	PBLUESCRIPT
33	Nervous (0.216) Reproductive(0.235) Cardiovascular (0.118)	Cell proliferation (0.530) Inflammation (0.352)	pINCY
34	Reproductive (0.293) Gastrointestinal (0.192)	Cell proliferation (0.641) Inflammation (0.335)	pINCY
35	Reproductive (0.284) Nervous (0.210) Cardiovascular (0.1213)	Cell proliferation (0.729) Inflammation (0.272)	pINCY
36	Nervous (0.529) Developmental (0.118) Gastrointestinal (0.118)	Cell proliferation (0.588) Neurological (0.118) Inflammation (0.118)	pINCY
37	Hematopoietic/Immune (0.268) Reproductive (0.244) Nervous (0.122)	Inflammation (0.488) Cell Proliferative (0.415)	PBLUESCRIPT
38	Reproductive (0.400) Hematopoietic/Immune (0.160) Nervous (0.160)	Cell proliferation (0.600) Inflammation (0.320)	pINCY
39	Cardiovascular (0.312) Reproductive (0.312) Developmental (0.188)	Cell proliferation (0.938) Inflammation (0.125)	pINCY
40	Nervous (0.400) Gastrointestinal (0.267) Developmental (0.133)	Cell proliferation (0.733) Neurological (0.133) Inflammation (0.133)	pINCY
41	Gastrointestinal (0.267) Nervous (0.233) Reproductive (0.167)	Inflammation (0.533) Cell proliferation (0.534)	pSPORT1

Table 3 cont.

Nucleotide SEQ ID NO:	Tissue Expression (Fraction of Total)	Disease or Condition (Fraction of Total)	Vector
42	Musculoskeletal (0.500) Developmental (0.167) Gastrointestinal (0.167)	Cancer (0.834) Inflammation (0.167)	PBLUESCRIPT
43	Reproductive (0.240) Nervous (0.151) Gastrointestinal (0.135)	Cell proliferation (0.536) Inflammation (0.417)	pSPORT1
44	<pre>Hematopoietic/Immune (0.278) Nervous (0.222) Dermatologic (0.111)</pre>	Cell proliferation (0.444) Inflammation (0.389)	pincy
45	Hematopoietic/Immune (0.500) Gastrointestinal (0.125) Nervous (0.125)	Inflammation (0.500) Cell proliferative (0.500)	PBLUESCRIPT
46	Nervous (0.220) Reproductive (0.213) Hematopoietic/Immune (0.140)	Cell proliferation (0.573) Inflammation (0.380)	pSPORT1
47	Hematopoietic/Immune (0.190) Gastrointestinal (0.165) Nervous (0.139)	Cell proliferation (0.582) Inflammation (0.354)	pSPORT1

Table 3 cont.

Nucleotide	Tissue Expression	Disease or Condition	Vector
SEQ ID NO:	(Fraction of Total)	(Fraction of Total)	
48	Nervous (0.333) Reproductive (0.333) Hematopoietic/Immune (0.111)	Cancer (0.444) Inflammation (0.222) Neurological (0.111)	PBLUESCRIPT
49	Nervous (0.724) Cardiovascular (0.103)	Inflammation (0.276) Cancer (0.241) Neurological (0.172)	pINCY
50	Reproductive (0.235) Hematopoietic/Immune (0.188) Gastrointestinal (0.129)	Cancer (0.447) Inflammation (0.282) Fetal (0.153)	pincy
51	Nervous (0.368) Developmental (0.158) Gastrointestinal (0.105)	Cancer (0.368) Fetal (0.211) Inflammation (0.105)	pSPORT1
52	Cardiovascular (0.312) Hematopoietic/Immune (0.312) Reproductive (0.158)	Fetal (0.688) Cancer (0.421) Inflammation (0.125)	pincy
53	Reproductive (0.412) Nervous (0.235) Developmental (0.118)	Cancer (0.471) Fetal (0.235) Inflammation (0.235)	pINCY
54	Nervous (0.714) Cardiovascular (0.107)	Cancer (0.250) Inflammation (0.250) Neurological (0.179)	pincy

Table 3 cont.

	ы		
Nucleotide SEQ ID NO:	Tissue Expression (Fraction of Total)	Disease or Condition (Fraction of Total)	PBLUESCRIPT
55	Reproductive (0.533) Nervous (0.133)	Cell proliferation (0.601) Inflammation (0.270)	PBLUESCRIPT
95	<pre>Hematopoietic/Immune (0.278) Nervous (0.222) Reproductive (0.154)</pre>	Cell proliferation (0.388) Inflammation (0.333) Neurological (0.111)	PBLUESCRIPT
57	Hematopoietic/Immune (0.211) Cardiovascular (0.193) Nervous (0.175)	Cell proliferation (0.474) Inflammation (0.491)	PBLUESCRIPT
28	Reproductive (0.286) Cardiovascular (0.229) Musculoskeletal (0.143)	Cell proliferation (0.715) Inflammation (0.200)	pINCY
59	Reproductive (0.253) Gastrointestinal (0.211) Nervous (0.147)	Cancer and Cell proliferation (0.684) Inflammation and Immune Response (0.242)	psPORT1
09	Nervous (0.667) Reproductive (0.333)	Cancer (1.000)	pSPORT1
61	Reproductive (0.357) Cardiovascular (0.179) Nervous (0.125)	Cancer and Cell proliferation (0.642) Inflammation and Immune Response (0.232)	pSPORT1
62	Nervous (0.228) Reproductive (0.175) Cardiovascular (0.158) Hematopoietic/Immune (0.158)	Cancer (0.368) Inflammation and Immune Response (0.263) Fetal (0.211)	pINCY

TABLE 4

Polynucleotide		
SEQ ID NO:	Library	Library Comment
32	BMARNOT02	Library was constructed using RNA isolated from the bone marrow of 24 male and female Caucasian donors, 16 to 70 years old.
33	SININOT01	Library was constructed using RNA isolated from ileum tissue removed from the small intestine of a 4-year-old Caucasian female, who died from a closed head injury. Patient history included jaundice as a baby. Previous surgeries included a double hernia repair
34	SPLNFET02	Library was constructed using RNA isolated from spleen tissue removed from a Caucasian male fetus, who died at 23 weeks' gestation from premature birth. Family history included diabetes.
35	OVARTUT02	Library was constructed using RNA isolated from ovarian tumor tissue removed from a 51-year-old Caucasian female during an exploratory laparotomy, total abdominal hysterectomy, salpingo-oophorectomy, and an incidental appendectomy. Pathology indicated mucinous cystadenoma presenting as a multiloculated neoplasm involving the entire left ovary. The right ovary contained a follicular cyst and a hemorrhagic corpus luteum. The uterus showed proliferative endometrium and a single intramural leiomyoma. The peritoneal biopsy indicated benign glandular inclusions consistent with endosalpingiosis. The patient presented with abnormal weight gain and ascites. Patient history included depressive disorder, joint pain, allergies, alcohol use, and a normal delivery. Family history included atherosclerotic coronary artery disease, benign hypertension, breast cancer and uterine cancer.

Polynucleotide SEQ ID NO:	Library	Library Comment
36	PANCTUT-01	library was constructed using RNA isolated from pancreatic tumor tissue removed from a 65-year-old Caucasian female during radical subtotal pancreatectomy. Pathology indicated an invasive grade 2 adenocarcinoma. Patient history included type II diabetes, osteoarthritis, cardiovascular disease, and benign neoplasm in the large bowel. Previous surgeries included a total splenectomy, cholecystectomy, and abdominal hysterectomy. Family history included cardiovascular disease, type II diabetes, and stomach cancer.
37	SMCBUNT01	library was constructed using RNA isolated from bronchial smooth muscle cell tissue removed from a 21-year-old Caucasian male.
38	UTRSTUT05	Library was constructed using RNA isolated from uterine tumor tissue removed from a 41-year-old Caucasian female during a vaginal hysterectomy with dilation and curettage. Pathology indicated uterine leiomyoma. The endometrium was secretory and contained fragments of endometrial polyps. Benign endo- and ectocervical mucosa were identified in the endocervix. Patient history included a ventral hernia and a benign ovarian neoplasm.
39	UTRSTUT04	library was constructed using RNA isolated from uterine tumor tissue removed from a 34-year-old Caucasian female during a hysteroscopy and an exploratory laparotomy with dilation and curettage. Pathology indicated an endometrial polyp, subserosal leiomyoma, and fragments of leiomyoma. Family history included hyperlipidemia, depressive disorder, benign hypertension, cerebrovascular disease, arteriosclerotic cardiovascular disease, and type II diabetes.

Polynucleotide SEQ ID NO:	Library	Library Comment
46	BRSTTUT03	library was constructed using RNA isolated from breast tumor tissue removed from a 58-year-old Caucasian female during a unilateral extended simple mastectomy. Pathology indicated multicentric invasive grade 4 lobular carcinoma. The mass was identified in the upper outer quadrant, and three separate nodules were found in the lower outer quadrant of the left breast. Patient history included skin cancer, rheumatic heart disease, osteoarthritis, and tuberculosis. Family history included cerebrovascular disease, coronary artery aneurysm, breast cancer, prostate cancer, atherosclerotic coronary artery disease, and type I diabetes.
47	BRSTNOT05	library was constructed using RNA isolated from breast tissue removed from a 58-year-old Caucasian female during a unilateral extended simple mastectomy. Pathology for the associated tumor tissue indicated multicentric invasive grade 4 lobular carcinoma. Patient history included skin cancer, rheumatic heart disease, osteoarthritis, and tuberculosis. Family history included cerebrovascular and cardiovascular disease, breast and prostate cancer, and type I diabetes.

Polynucleotide SEQ ID NO:	Library	Library Comment
φ 00	SPLANOT02	The library was constructed using RNA isolated from the spleen tissue of a 29-year-old Caucasian male, who died from head trauma. Serologies were positive for cytomegalovirus (CMV). Patient history included alcohol, marijuana, and tobacco use.
49	BRAITUT08	The library was constructed using RNA isolated from brain tumor tissue removed from the left frontal lobe of a 47-year-old Caucasian male during excision of cerebral meningeal tissue. Pathology indicated grade 4 fibrillary astrocytoma with focal tumoral radionecrosis. Patient history included cerebrovascular disease, deficiency anemia, hyperlipidemia, epilepsy, and tobacco use. Family history included cerebrovascular disease and a malignant prostate neoplasm.
5.0	PANCTUT01	The library was constructed using RNA isolated from pancreatic tumor tissue removed from a 65-year-old Caucasian female during radical subtotal pancreatectomy. Pathology indicated an invasive grade 2 adenocarcinoma. Patient history included type II diabetes, osteoarthritis, cardiovascular disease, benign neoplasm in the large bowel, and a cataract. Previous surgeries included a total splenectomy, cholecystectomy, and abdominal hysterectomy. Family history included cardiovascular disease, type II diabetes, and stomach cancer.
51	BRAITUT02	The library was constructed using RNA isolated from brain tumor tissue removed from the frontal lobe of a 58-year-old Caucasian male during excision of a cerebral meningeal lesion. Pathology indicated a grade 2 metastatic hypernephroma. Patient history included a grade 2 renal cell carcinoma, insomnia, and chronic airway obstruction. Family history included a malignant neoplasm of the kidney.

TABLE 4 cont.

Polynucleotide SEQ ID NO:	Library	Library Comment
52	THP1NOT03	The library was constructed using RNA isolated from untreated THP-1 cells. THP-1 (ATCC TIB 202) is a human promonocyte line derived from the peripheral blood of a 1-year-old Caucasian male with acute monocytic leukemia (ref: Int. J. Cancer (1980) 26:171).
53	BRSTNOT12	The library was constructed using RNA isolated from diseased breast tissue removed from a 32-year-old Caucasian female during a bilateral reduction mammoplasty. Pathology indicated nonproliferative fibrocystic disease. Family history included cardiovascular disease.
54	MUSCNOT07	The library was constructed using RNA isolated from muscle tissue removed from the forearm of a 38-year-old Caucasian female during a soft tissue excision. Pathology for the associated tumor tissue indicated intramuscular hemangioma. Family history included breast cancer, benign hypertension, cerebrovascular disease, colon cancer, and type II diabetes.
55	HUVESTB01	Library was constructed using RNA isolated from shear-stressed HUV-EC-C (ATCC CRL 1730) cells. HUV-EC-C is an endothelial cell line derived from the vein of a normal human umbilical cord (ref:PNAS 81:6413).
56	THYMNOT02	ibrary was constructed using polyA RNA isolated from thymus tissue removed from a 3-year-old Caucasian male, who died from drowning.
57	CARDNOT01	Library was constructed using RNA isolated from the cardiac muscle of a 65-year-old Caucasian male, who died from a self-inflicted gunshot wound.

TABLE 4 cont.

Polynucleotide SEQ ID NO:	Library	Library Comment
58	UTRSNOT12	Library was constructed using RNA isolated from uterine myometrial tissue removed from a 41-year-old Caucasian female during a vaginal hysterectomy with a dilatation and curettage. The endometrium was secretory and contained fragments of endometrial polyps. Benign endo- and ectocervical mucosa were identified in the endocervix. Pathology for the associated tumor tissue indicated uterine leiomyoma. The patient presented with an unspecified menstrual disorder. Patient history included ventral hernia, normal delivery, a benign ovarian neoplasm, and tobacco abuse. Previous surgeries included a bilateral destruction of fallopian tubes, removal of a solitary ovary, and an exploratory laparotomy.
59	BEPINOT01	Library was constructed using RNA isolated from a bronchial epithelium primary cell line derived from a 54-year-old Caucasian male.
09	PGANNOT01	Library was constructed using RNA isolated from paraganglionic tumor tissue removed from the intra-abdominal region of a 46-year-old Caucasian male during exploratory laparotomy. Pathology indicated a benign paraganglioma and association with a grade 2 renal cell carcinoma, clear cell type.
61	BEPINOT01	Library was constructed using RNA isolated from a bronchial epithelium primary cell line derived from a 54-year-old Caucasian male.
62	DRGLNOT01	Library was constructed using RNA isolated from dorsal root ganglion tissue removed from the low thoracic/high lumbar region of a 32-year- old Caucasian male who died from acute pulmonary edema and bronchopneumonia, bilateral pleural and pericardial effusions, and malignant lymphoma (natural killer cell type). Patient history included probable cytomegalovirus infection, hepatic congestion and steatosis, splenomegaly, hemorrhagic cystitis, thyroid hemorrhage, and Bell's palsy.

Table 5

Program	Description	Reference	Parameter Threshold
ABI FACTURA	A program that removes vector sequences and masks ambiguous bases in nucleic acid sequences.	Perkin-Elmer Applied Biosystems, Foster City, CA.	
ABI/PARACEL FDF	A Fast Data Finder useful in comparing and annotating amino acid or nucleic acid sequences.	Perkin-Elmer Applied Biosystems, Foster City, CA; Paracel Inc., Pasadena, CA.	Mismatch <50%
ABI AutoAssembler	A program that assembles nucleic acid sequences.	Perkin-Elmer Applied Biosystems, Foster City, CA.	
BLAST	A Basic Local Alignment Search Tool useful in sequence similarity search for amino acid and nucleic acid sequences. BLAST includes five functions: blastp, blastn,	Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410; Altschul, S.F. et al. (1997) Nucleic Acids Res. 25: 3389-3402.	ESTs: Probability value= 1.0E-8 or less Full Length sequences: Probability
73-	blastx, tblastn, and tblastx.		value= 1.0E-10 or less
FASTA	A Pearson and Lipman algorithm that searches for similarity between a query sequence and a group of sequences of the same type. FASTA comprises as least five functions: fasta, tfasta, fastx, tfastx, and ssearch.	Pearson, W.R. and D.J. Lipman (1988) Proc. Natl. Acad Sci. 85:2444-2448; Pearson, W.R. (1990) Methods Enzymol. 183: 63-98; and Smith, T.F. and M. S. Waterman (1981) Adv. Appl. Math. 2:482-489.	ESTs: fasta E value=1.06E-6 Assembled ESTs: fasta Identity= 95% or greater and Match length=200 bases or greater; fastx E value=1.0E-8 or less Full Length sequences: fastx score=100 or greater
BLIMPS	A BLocks IMProved Searcher that matches a sequence against those in BLOCKS, PRINTS, DOMO, PRODOM, and PFAM databases to search for gene families, sequence homology, and structural fingerprint regions.	Henikoff, S and J.G. Henikoff, Nucl. Acid Res., 19:6565-72, 1991. J.G. Henikoff and S. Henikoff (1996) Methods Enzymol. 266:88- 105; and Attwood, T.K. et al. (1997) J. Chem. Inf. Comput. Sci. 37: 417-424.	Score=1000 or greater, Ratio of Score/Strength = 0.75 or larger, and, if applicable, Probability value= 1.0E-3 or less
HMMER	An algorithm for searching a query sequence against hidden Markov model (HMM)-based databases of protein family consensus sequences, such as PFAM.	Krogh, A. et al. (1994) J. Mol. Biol., 235:1501-1531; Sonnhammer, E.L.L. et al. (1988) Nucleic Acids Res. 26:320-322.	Score=10-50 bits for PFAM hits, depending on individual protein families

Table 5 (cont.)

Parameter Threshold	Normalized quality score 2 GCG-specified "HIGH" value for that particular Prosite motif. Generally, score=1.4-2.1.		Score= 120 or greater; Match length= 56 or greater		Score=3.5 or greater	
Reference	Gribskov, M. et al. (1988) CABIOS 4:61-66; Gribskov, et al. (1989) Methods Enzymol. 183:146-159; Bairoch, A. et al. (1997) Nucleic Acids Res. 25: 217-221.	Ewing, B. et al. (1998) Genome Res. 8:175-185; Ewing, B. and P. Green (1998) Genome Res. 8:186- 194.	Smith, T.F. and M. S. Waterman (1981) Adv. Appl. Math. 2:482-489; Smith, T.F. and M. S. Waterman (1981) J. Mol. Biol. 147:195-197; and Green, P., University of Washington, Seattle, WA.	Gordon, D. et al. (1998) Genome Res. 8:195-202.	Nielson, H. et al. (1997) Protein Engineering 10:1-6; Claverie, J.M. and S. Audic (1997) CABIOS 12: 431-439.	Bairoch et al. <u>supra;</u> Wisconsin Package Program Manual, version 9, page M51-59, Genetics Computer Group, Madison, W1.
Description	An algorithm that searches for structural and sequence motifs in protein sequences that match sequence patterns defined in Prosite.	A base-calling algorithm that examines automated sequencer traces with high sensitivity and probability.	A Phils Revised Assembly Program including SWAT and CrossMatch, programs based on efficient implementation of the Smith-Waterman algorithm, useful in searching sequence homology and assembling DNA sequences.	A graphical tool for viewing and editing Phrap assemblies	A weight matrix analysis program that scans protein sequences for the presence of secretory signal peptides.	A program that searches amino acid sequences for patterns that matched those defined in Prosite.
Program	ProfileScan	Phred	वे स्यास - 74-	Consed	SPScan	Motifs



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- 1. A substantially purified polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-31, and fragments thereof.
- 5 2. A substantially purified variant having at least 90% amino acid sequence identity to the amino acid sequence of claim 1.
 - 3. An isolated and purified polynucleotide encoding the polypeptide of claim 1.
 - 4. An isolated and purified polynucleotide variant having at least 80% polynucleotide sequence identity to the polynucleotide of claim 3.
- 5. An isolated and purified polynucleotide which hybridizes under stringent conditions to the polynucleotide of claim 3.
 - 6. An isolated and purified polynucleotide having a sequence which is complementary to the polynucleotide of claim 3.
 - 7. A method for detecting a polynucleotide, the method comprising the steps of:
 - (a) hybridizing the polynucleotide of claim 6 to at least one nucleic acid in a sample, thereby forming a hybridization complex; and
 - (b) detecting the hybridization complex, wherein the presence of the hybridization complex correlates with the presence of the polynucleotide in the sample.
- 8. The method of claim 7 further comprising amplifying the polynucleotide prior to hybridization.
 - 9. An isolated and purified polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:32-62 and fragments thereof.
 - 10. An isolated and purified polynucleotide variant having at least 80% polynucleotide sequence identity to the polynucleotide of claim 9.
- 25 11. An isolated and purified polynucleotide having a sequence which is complementary to the polynucleotide of claim 9.
 - 12. An expression vector comprising at least a fragment of the polynucleotide of claim3.
 - 13. A host cell comprising the expression vector of claim 12.
 - 14. A method for producing a polypeptide, the method comprising the steps of:
 - a) culturing the host cell of claim 13 under conditions suitable for the expression of the polypeptide; and
 - b) recovering the polypeptide from the host cell culture.
- 15. A pharmaceutical composition comprising the polypeptide of claim 1 in conjunction with a suitable pharmaceutical carrier.
 - 16. A purified antibody which specifically binds to the polypeptide of claim 1.

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PCT/US99/17132



- 17. A purified agonist of the polypeptide of claim 1.
- 18. A purified antagonist of the polypeptide of claim 1.
- 19. A method for treating or preventing a disorder associated with decreased expression or activity of PHSP, the method comprising administering to a subject in need of such treatment an
 5 effective amount of the pharmaceutical composition of claim 15.
 - 20. A method for treating or preventing a disorder associated with increased expression or activity of PHSP, the method comprising administering to a subject in need of such treatment an effective amount of the antagonist of claim 18.

SEQUENCE LISTING

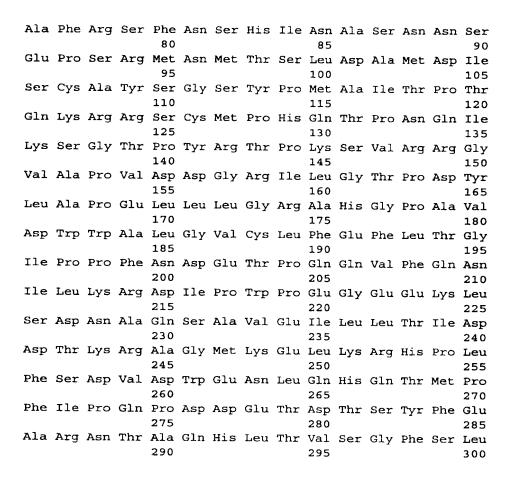
<110> INYCTE PHARMACEUTICALS, INC. HILLMAN, Jennifer L. LAL, Preeti TANG, Y. Tom CORLEY, Neil C. GUEGLER, Karl J. BAUGHN, Mariah R. PATTERSON, Chandra BANDMAN, Olga AU-YOUNG, Janice GORGONE, Gina A. YUE, Henry AZIMZAI, Yalda REDDY, Roopa LU, Dyung Aina M. SHIH, Leo L. <120> PHOSPHORYLATION EFFECTORS <130> PF-0565 PCT <140> To Be Assigned <141> Herewith <150> 09/123,494; unassigned; 09/152,814; unassigned; 09/173,482; unassigned; 60/106, 889; 60/109, 093; 60/113, 796; <151> 1998-07-28; 1998-07-28; 1998-09-14; 1998-09-14; 1998-10-14; 1998-10-14;1998-11-03; 1998-11-19; 1998-12-22 <160> 61 <170> PERL Program <210> 1 <211> 300 <212> PRT <213> Homo sapiens <220> <221> misc_feature <223> Incyte Clone Number: 132240 <400> 1 Met Glu Ser Pro Leu Glu Ser Gln Pro Leu Asp Ser Asp Arg Ser 10 Ile Lys Glu Ser Ser Phe Glu Glu Ser Asn Ile Glu Asp Pro Leu 20 Ile Val Thr Pro Asp Cys Gln Glu Lys Thr Ser Pro Lys Gly Val 40 45 Glu Asn Pro Ala Val Gln Glu Ser Asn Gln Lys Met Leu Gly Pro 50 55 Pro Leu Glu Val Leu Lys Thr Leu Ala Ser Lys Arg Asn Ala Val

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Leu Lys Ala Asp Pro Glu Glu Leu Phe Thr Lys Leu Glu Lys Ile 25 Gly Lys Gly Ser Phe Gly Glu Val Phe Lys Gly Ile Asp Asn Arg Thr Gln Lys Val Val Ala Ile Lys Ile Ile Asp Leu Glu Glu Ala Glu Asp Glu Ile Glu Asp Ile Gln Gln Glu Ile Thr Val Leu Ser Gln Cys Asp Ser Pro Tyr Val Thr Lys Tyr Tyr Gly Ser Tyr Leu 85 Lys Asp Thr Lys Leu Trp Ile Ile Met Glu Tyr Leu Gly Gly 95 100 Ser Ala Leu Asp Leu Leu Glu Pro Gly Arg Leu Asp Glu Thr Gln 110 115 Ile Ala Thr Ile Leu Arg Glu Ile Leu Lys Gly Leu Asp Tyr Leu 125 130 His Ser Glu Lys Lys Ile His Arg Asp Ile Lys Ala Ala Asn Val 145 Leu Leu Ser Glu His Gly Glu Val Lys Leu Ala Asp Phe Gly Val 155 160 Ala Gly Gln Leu Thr Asp Thr Gln Ile Lys Arg Asn Thr Phe Val 170 175 Gly Thr Pro Phe Trp Met Ala Pro Glu Val Ile Lys Gln Ser Ala 185 190 Tyr Asp Ser Lys Ala Asp Ile Trp Ser Leu Gly Ile Thr Ala Ile 200 205 Glu Leu Ala Arg Gly Glu Pro Pro His Ser Glu Leu His Pro Met 215 220 Lys Val Leu Phe Leu Ile Pro Lys Asn Asn Pro Pro Thr Leu Glu 230 235 Gly Asn Tyr Ser Lys Pro Leu Lys Glu Phe Val Glu Ala Cys Leu 245 Asn Lys Glu Pro Ser Phe Arg Pro Thr Ala Lys Glu Leu Leu Lys

His Lys Phe Ile Leu Arg Asn Ala Lys Lys Thr Ser Tyr Leu Thr

275

265

280

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Glu Leu Ile Asp Arg Tyr Lys Arg Trp Lys Ala Glu Gln Ser His
                290
                                    295
Asp Asp Ser Ser Ser Glu Asp Ser Asp Ala Glu Thr Asp Gly Gln
                305
                                    310
Ala Ser Gly Gly Ser Asp Ser Gly Asp Trp Ile Phe Thr Ile Arg
                                    325
Glu Lys Asp Pro Lys Asn Leu Glu Asn Gly Ala Leu Gln Pro Ser
                335
                                    340
Asp Leu Asp Arg Asn Lys Met Lys Asp Ile Pro Lys Arg Pro Phe
                350
Ser Gln Cys Leu Ser Thr Ile Ile Ser Pro Leu Phe Ala Glu Leu
                                    370
Lys Glu Lys Ser Gln Ala Cys Gly Gly Asn Leu Gly Ser Ile Glu
                380
                                    385
Glu Leu Arg Gly Ala Ile Tyr Leu Ala Glu Glu Ala Cys Pro Gly
                395
                                    400
Ile Ser Asp Thr Met Val Ala Gln Leu Val Gln Arg Leu Gln Arg
                410
                                    415
Tyr Ser Leu Ser Gly Gly Gly Thr Ser Ser His
                425
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<210> 4

<211> 218

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone Number: 2594943

<400> 4

Met Asn Cys Arg Ser Glu Val Leu Glu Val Ser Val Glu Gly Arg Gln Val Glu Glu Ala Met Leu Ala Val Leu His Thr Val Leu Leu His Arg Ser Thr Gly Lys Phe His Tyr Lys Lys Glu Gly Thr Tyr Ser Ile Gly Thr Val Gly Thr Gln Asp Val Asp Cys Asp Phe Ile Asp Phe Thr Tyr Val Arg Val Ser Ser Glu Glu Leu Asp Arg Ala Leu Arg Lys Val Val Gly Glu Phe Lys Asp Ala Leu Arg Asn Ser 85 Gly Gly Asp Gly Leu Gly Gln Met Ser Leu Glu Phe Tyr Gln Lys 95 100 Lys Lys Ser Arg Trp Pro Phe Ser Asp Glu Cys Ile Pro Trp Glu 110 115 Val Trp Thr Val Lys Val His Val Val Ala Leu Ala Thr Glu Gln 125 130 Glu Arg Gln Ile Cys Arg Glu Lys Val Gly Glu Lys Leu Cys Glu 140 145 150 Lys Ile Ile Asn Ile Val Glu Val Met Asn Arg His Glu Tyr Leu 155 160 165 Pro Lys Met Pro Thr Gln Ser Glu Val Asp Asn Val Phe Asp Thr 170 175 180

```
Gly Leu Arg Asp Val Gln Pro Tyr Leu Tyr Lys Ile Ser Phe Gln
                185
Ile Thr Asp Ala Leu Gly Thr Ser Val Thr Thr Met Arg Arg
                                   205
Leu Ile Lys Asp Thr Leu Ala Leu
               215
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<210> 5 <211> 474 <212> PRT <213> Homo sapiens <220> <221> misc_feature <223> Incyte Clone Number: 1513871 <400> 5 Met Ile Met Asn Lys Met Lys Asn Phe Lys Arg Arg Phe Ser Leu 10 Ser Val Pro Arg Thr Glu Thr Ile Glu Glu Ser Leu Ala Glu Phe 20 25 Thr Glu Gln Phe Asn Gln Leu His Asn Arg Arg Asn Glu Asn Leu 35 Gln Leu Gly Pro Leu Gly Arg Asp Pro Pro Gln Glu Cys Ser Thr 50 Phe Ser Pro Thr Asp Ser Gly Glu Glu Pro Gly Gln Leu Ser Pro 65 Gly Val Gln Phe Gln Arg Arg Gln Asn Gln Arg Arg Phe Ser Met 80 Glu Asp Val Ser Lys Arg Leu Ser Leu Pro Met Asp Ile Arg Leu 95 Pro Gln Glu Phe Leu Gln Lys Leu Gln Met Glu Ser Pro Asp Leu 115 Pro Lys Pro Leu Ser Arg Met Ser Arg Arg Ala Ser Leu Ser Asp 130 Ile Gly Phe Gly Lys Leu Glu Thr Tyr Val Lys Leu Asp Lys Leu 145 Gly Glu Gly Thr Tyr Ala Thr Val Phe Lys Gly Arg Ser Lys Leu 160 Thr Glu Asn Leu Val Ala Leu Lys Glu Ile Arg Leu Glu His Glu 170 175 Glu Gly Ala Pro Cys Thr Ala Ile Arg Glu Val Ser Leu Leu Lys 185 190 Asn Leu Lys His Ala Asn Ile Val Thr Leu His Asp Leu Ile His 200 205 Thr Asp Arg Ser Leu Thr Leu Val Phe Glu Tyr Leu Asp Ser Asp 215 220 Leu Lys Gln Tyr Leu Asp His Cys Gly Asn Leu Met Ser Met His 230 235 Asn Val Lys Ile Phe Met Phe Gln Leu Leu Arg Gly Leu Ala Tyr 245 250 Cys His His Arg Lys Ile Leu His Arg Asp Leu Lys Pro Gln Asn

265

280

Leu Leu Ile Asn Glu Arg Gly Glu Leu Lys Leu Ala Asp Phe Gly

260

275

```
Leu Ala Arg Ala Lys Ser Val Pro Thr Lys Thr Tyr Ser Asn Glu
                290
                                     295
Val Val Thr Leu Trp Tyr Arg Pro Pro Asp Val Leu Leu Gly Ser
                305
                                     310
Thr Glu Tyr Ser Thr Pro Ile Asp Met Trp Gly Val Gly Cys Ile
His Tyr Glu Met Ala Thr Gly Arg Pro Leu Phe Pro Gly Ser Thr
                                     340
Val Lys Glu Glu Leu His Leu Ile Phe Arg Leu Leu Gly Thr Pro
Thr Glu Glu Thr Trp Pro Gly Val Thr Ala Phe Ser Glu Phe Arg
                                    370
Thr Tyr Ser Phe Pro Cys Tyr Leu Pro Gln Pro Leu Ile Asn His
                380
                                    385
Ala Pro Arg Leu Asp Thr Asp Gly Ile His Leu Leu Ser Ser Leu
                395
                                    400
Leu Leu Tyr Glu Ser Lys Ser Arg Met Ser Ala Glu Ala Ala Leu
                                    415
Ser His Ser Tyr Phe Arg Ser Leu Gly Glu Arg Val His Gln Leu
                425
                                    430
Glu Asp Thr Ala Ser Ile Phe Ser Leu Lys Glu Ile Gln Leu Gln
                440
                                     445
Lys Asp Pro Gly Tyr Arg Gly Leu Ala Phe Gln Gln Pro Gly Arg
                455
                                    460
Gly Lys Asn Arg Arg Gln Ser Ile Phe
                470
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<210> 6

<211> 540

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone Number: 156108

<400> 6

Met Asn Gly Glu Ala Ile Cys Ser Ala Leu Pro Thr Ile Pro Tyr His Lys Leu Ala Asp Leu Arg Tyr Leu Ser Arg Gly Ala Ser Gly Thr Val Ser Ser Ala Arg His Ala Asp Trp Arg Val Gln Val Ala 40 Val Lys His Leu His Ile His Thr Pro Leu Leu Asp Ser Glu Arg 50 Lys Asp Val Leu Arg Glu Ala Glu Ile Leu His Lys Ala Arg Phe Ser Tyr Ile Leu Pro Ile Leu Gly Ile Cys Asn Glu Pro Glu Phe 80 85 Leu Gly Ile Val Thr Glu Tyr Met Pro Asn Gly Ser Leu Asn Glu 95 100 Leu Leu His Arg Lys Thr Glu Tyr Pro Asp Val Ala Trp Pro Leu 110 115 Arg Phe Arg Ile Leu His Glu Ile Ala Leu Gly Val Asn Tyr Leu

				125					130					135
His	Asn	Met	Thr	Pro 140	Pro	Leu	Leu	His	His 145	Asp	Leu	Lys	Thr	Gln 150
Asn	Ile	Leu	Leu	Asp 155	Asn	Glu	Phe	His	Val 160	Lys	Ile	Ala	Asp	Phe 165
Gly	Leu	Ser	Lys	Trp 170	Arg	Met	Met	Ser		Ser	Gln	Ser	Arg	
Ser	Lys	Ser	Ala	Pro 185	Glu	Gly	Gly	Thr		Ile	Tyr	Met	Pro	
Glu	Asn	Tyr	Glu	Pro 200	Gly	Gln	Lys	Ser		Ala	Ser	Ile	Lys	
Asp	Ile	Tyr	Ser	Tyr 215	Ala	Val	Ile	Thr		Glu	Val	Leu	Ser	
Lys	Gln	Pro	Phe	Glu 230	Asp	Val	Thr	Asn	Pro 235	Leu	Gln	Ile	Met	Tyr 240
Ser	Val	Ser	Gln	Gly 2 4 5	His	Arg	Pro	Val		Asn	Glu	Glu	Ser	
Pro	Tyr	Asp	Ile	Pro 260	His	Arg	Ala	Arg		Ile	Ser	Leu	Ile	
Ser	Gly	Trp	Ala	Gln 275	Asn	Pro	Asp	Glu		Pro	Ser	Phe	Leu	
Cys	Leu	Ile	Glu	Leu 290	Glu	Pro	Val	Leu		Thr	Phe	Glu	Glu	
Thr	Phe	Leu	Glu		Val	Ile	Gln	Leu		Lys	Thr	Lys	Leu	
Ser	Val	Ser	Ser	Ala 320	Ile	His	Leu	Cys		Lys	Lys	Lys	Met	Glu 330
Leu	Ser	Leu	Asn		Pro	Val	Asn	His		Pro	Gln	Glu	Glu	
Cys	Gly	Ser	Ser		Leu	His	Glu	Asn		Gly	Ser	Pro	Glu	
Ser	Arg	Ser	Leu		Ala	Pro	Gln	Asp		Asp	Phe	Leu	Ser	
Lys	Ala	Gln	Asp		Tyr	Phe	Met	Lys		His	His	Cys	Pro	
Asn	His	Ser	Trp	Asp 395	Ser	Thr	Ile	Ser		Ser	Gln	Arg	Ala	
Phe	Cys	Asp	His	Lys 410	Thr	Thr	Pro	Cys	Ser 415	Ser	Ala	Ile	Ile	Asn 420
Pro	Leu	Ser	Thr	Ala 425	Gly	Asn	Ser	Glu	Arg 430	Leu	Gln	Pro	Gly	Ile 435
Ala	Gln	Gln	Trp	Ile 440	Gln	Ser	Lys	Arg	Glu 445	Asp	Ile	Val	Asn	Gln 450
Met	Thr	Glu	Ala	Cys 455	Leu	Asn	Gln	Ser	Leu 460	Asp	Ala	Leu	Leu	Ser 465
Arg	Asp	Leu	Ile	Met 470	Lys	Glu	Asp	Tyr		Leu	Val	Ser	Thr	Lys 480
Pro	Thr	Arg	Thr	Ser 485	Lys	Val	Arg	Gln		Leu	Asp	Thr	Thr	
lle	Gln	Gly	Glu		Phe	Ala	Lys	Val		Val	Gln	Lys	Leu	
Asp	Asn	Lys	Gln		Gly	Leu	Gln	Pro		Pro	Glu	Ile	Leu	
Val	Ser	Arg	Ser		Ser	Leu	Asn	Leu		Gln	Asn	Lys	Ser	

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<211> 454
<212> PRT
<213> Homo sapiens
<220>
<221> misc feature
<223> Incyte Clone Number: 2883243
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Ala Lys Thr Asp Ile Asn Cys Gly Thr Asp Leu Met Phe Tyr Ile
                                     25
Glu Met Asp Pro Pro Ala Leu Pro Pro Lys Pro Pro Lys Pro Thr
                 35
                                     40
Thr Val Ala Asn Asn Gly Met Asn Asn Asn Met Ser Leu Gln Asp
                                     55
Ala Glu Trp Tyr Trp Gly Asp Ile Ser Arg Glu Glu Val Asn Glu
                                     70
Lys Leu Arg Asp Thr Ala Asp Gly Thr Phe Leu Val Arg Asp Ala
                 80
                                     85
Ser Thr Lys Met His Gly Asp Tyr Thr Leu Thr Leu Arq Lys Gly
                 95
                                    100
Gly Asn Asn Lys Leu Ile Lys Ile Phe His Arg Asp Gly Lys Tyr
                110
                                    115
Gly Phe Ser Asp Pro Leu Thr Phe Ser Ser Val Val Glu Leu Ile
                125
                                    130
Asn His Tyr Arg Asn Glu Ser Leu Ala Gln Tyr Asn Pro Lys Leu
                140
                                    145
Asp Val Lys Leu Leu Tyr Pro Val Ser Lys Tyr Gln Gln Asp Gln
Val Val Lys Glu Asp Asn Ile Glu Ala Val Gly Lys Lys Leu His
Glu Tyr Asn Thr Gln Phe Gln Glu Lys Ser Arg Glu Tyr Asp Arg
Leu Tyr Glu Glu Tyr Thr Arg Thr Ser Gln Glu Ile Gln Met Lys
Arg Thr Ala Ile Glu Ala Phe Asn Glu Thr Ile Lys Ile Phe Glu
Glu Gln Cys Gln Thr Gln Glu Arg Tyr Ser Lys Glu Tyr Ile Glu
                                     235
Lys Phe Lys Arg Glu Gly Asn Glu Lys Glu Ile Gln Arg Ile Met
                245
                                     250
His Asn Tyr Asp Lys Leu Lys Ser Arg Ile Ser Glu Ile Ile Asp
                260
                                     265
Ser Arg Arg Leu Glu Glu Asp Leu Lys Lys Gln Ala Ala Glu
                 275
                                    280
Tyr Arg Glu Ile Asp Lys Arg Met Asn Ser Ile Lys Pro Asp Leu
                 290
                                     295
                                                         300
Ile Gln Leu Arg Lys Thr Arg Asp Gln Tyr Leu Met Trp Leu Thr
                 305
                                     310
Gln Lys Gly Val Arg Gln Lys Lys Leu Asn Glu Trp Leu Gly Asn
                 320
                                     325
Glu Asn Thr Glu Asp Gln Tyr Ser Leu Val Glu Asp Asp Glu Asp
                 335
                                     340
                                                         345
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Leu Pro His His Asp Glu Lys Thr Trp Asn Val Gly Ser Ser Asn 355 Arg Asn Lys Ala Glu Asn Leu Leu Arg Gly Lys Arg Asp Gly Thr 370 Phe Leu Val Arg Glu Ser Ser Lys Gln Gly Cys Tyr Ala Cys Ser 380 385 Val Val Val Asp Gly Glu Val Lys His Cys Val Ile Asn Lys Thr 395 400 Ala Thr Gly Tyr Gly Phe Ala Glu Pro Tyr Asn Leu Tyr Ser Ser 410 415 Leu Lys Glu Leu Val Leu His Tyr Gln His Thr Ser Leu Val Gln 425 430 His Asn Asp Ser Leu Asn Val Thr Leu Ala Tyr Pro Val Tyr Ala 440 Gln Gln Arg Arg

<210> 8

<211> 502

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone Number: 3173355

<400> 8

Met Phe Gly Thr Leu Leu Tyr Cys Phe Phe Leu Ala Thr Val Pro Ala Leu Ala Glu Thr Gly Gly Glu Arg Gln Leu Ser Pro Glu Lys Ser Glu Ile Trp Gly Pro Gly Leu Lys Ala Asp Val Val Leu 35 40 Pro Ala Arg Tyr Phe Tyr Ile Gln Ala Val Asp Thr Ser Gly Asn 50 55 Lys Phe Thr Ser Ser Pro Gly Glu Lys Val Phe Gln Val Lys Val Ser Ala Pro Glu Glu Gln Phe Thr Arg Val Gly Val Gln Val Leu 85 Asp Arg Lys Asp Gly Ser Phe Ile Val Arg Tyr Arg Met Tyr Ala 95 100 Ser Tyr Lys Asn Leu Lys Val Glu Ile Lys Phe Gln Gly Gln His 110 115 Val Ala Lys Ser Pro Tyr Ile Leu Lys Gly Pro Val Tyr His Glu 125 130 135 Asn Cys Asp Cys Pro Leu Gln Asp Ser Ala Ala Trp Leu Arg Glu 140 145 Met Asn Cys Pro Glu Thr Ile Ala Gln Ile Gln Arg Asp Leu Ala 155 160 His Phe Pro Ala Val Asp Pro Glu Lys Ile Ala Val Glu Ile Pro 170 175 Lys Arg Phe Gly Gln Arg Gln Ser Leu Cys His Tyr Thr Leu Lys 190 Asp Asn Lys Val Tyr Ile Lys Thr His Gly Glu His Val Gly Phe 205 Arg Ile Phe Met Asp Ala Ile Leu Leu Ser Leu Thr Arg Lys Val

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215
                                     220
                                                         225
Lys Met Pro Asp Val Glu Leu Phe Val Asn Leu Gly Asp Trp Pro
                230
                                     235
Leu Glu Lys Lys Ser Asn Ser Asn Ile His Pro Ile Phe Ser
                245
                                     250
Trp Cys Gly Ser Thr Asp Ser Lys Asp Ile Val Met Pro Thr Tyr
                                     265
Asp Leu Thr Asp Ser Val Leu Glu Thr Met Gly Arg Val Ser Leu
                275
Asp Met Met Ser Val Gln Ala Asn Thr Gly Pro Pro Trp Glu Ser
                290
Lys Asn Ser Thr Ala Val Trp Arg Gly Arg Asp Ser Arg Lys Glu
                305
Arg Leu Glu Leu Val Lys Leu Ser Arg Lys His Pro Glu Leu Ile
                320
                                     325
Asp Ala Ala Phe Thr Asn Phe Phe Phe Lys His Asp Glu Asn
                335
                                     340
Leu Tyr Gly Pro Ile Val Lys His Ile Ser Phe Phe Asp Phe Phe
                350
                                     355
Lys His Lys Tyr Gln Ile Asn Ile Asp Gly Thr Val Ala Ala Tyr
                365
                                     370
                                                         375
Arg Leu Pro Tyr Leu Leu Val Gly Asp Ser Val Val Leu Lys Gln
                380
                                    385
                                                         390
Asp Ser Ile Tyr Tyr Glu His Phe Tyr Asn Glu Leu Gln Pro Trp
                395
                                     400
                                                         405
Lys His Tyr Ile Pro Val Lys Ser Asn Leu Ser Asp Leu Leu Glu
                410
                                     415
Lys Leu Lys Trp Ala Lys Asp His Asp Glu Glu Ala Lys Lys Ile
                425
                                     430
Ala Lys Ala Gly Gln Glu Phe Ala Arg Asn Asn Leu Met Gly Asp
                440
                                     445
Asp Ile Phe Cys Tyr Tyr Phe Lys Leu Phe Gln Glu Tyr Ala Asn
                455
                                     460
Leu Gln Val Ser Glu Pro Gln Ile Arg Glu Gly Met Lys Arg Val
                470
                                     475
Glu Pro Gln Thr Glu Asp Asp Leu Phe Pro Cys Thr Cys His Arg
                485
Lys Lys Thr Lys Asp Glu Leu
<210> 9
<211> 282
<212> PRT
<213> Homo sapiens
<220>
<221> misc_feature
<223> Incyte Clone Number: 5116906
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Met Trp Ala Cys Gly Val Ile Leu Tyr Ile Leu Leu Val Gly Tyr
                                     10
Pro Pro Phe Trp Asp Glu Asp Gln His Arg Leu Tyr Gln Gln Ile
                 20
                                     25
Lys Ala Gly Ala Tyr Asp Phe Pro Ser Pro Glu Trp Asp Thr Val
                 35
                                      40
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Thr Pro Glu Ala Lys Asp Leu Ile Asn Lys Met Leu Thr Ile Asn 50 Pro Ala Lys Arg Ile Thr Ala Ser Glu Ala Leu Lys His Pro Trp 65 Ile Cys Gln Arg Ser Thr Val Ala Ser Met Met His Arg Gln Glu 80 85 Thr Val Asp Cys Leu Lys Lys Phe Asn Ala Arg Arg Lys Leu Lys 95 100 Gly Ala Ile Leu Thr Thr Met Leu Ala Thr Arg Asn Phe Ser Ala 110 115 Ala Lys Ser Leu Leu Lys Lys Pro Asp Gly Val Lys Glu Ser Thr 125 130 Glu Ser Ser Asn Thr Thr Ile Glu Asp Glu Asp Val Lys Ala Arg 140 145 Lys Gln Glu Ile Ile Lys Val Thr Glu Gln Leu Ile Glu Ala Ile 155 160 Asn Asn Gly Asp Phe Glu Ala Tyr Thr Lys Ile Cys Asp Pro Gly 175 Leu Thr Ala Phe Glu Pro Glu Ala Leu Gly Asn Leu Val Glu Gly 190 Met Asp Phe His Arg Phe Tyr Phe Glu Asn Ala Leu Ser Lys Ser 205 200 Asn Lys Pro Ile His Thr Ile Ile Leu Asn Pro His Val His Leu 220 Val Gly Asp Asp Ala Ala Cys Ile Ala Tyr Ile Arg Leu Thr Gln 230 235 Tyr Met Asp Gly Ser Gly Met Pro Lys Thr Met Gln Ser Glu Glu 250 245 Thr Arg Val Trp His Arg Arg Asp Gly Lys Trp Gln Asn Val His 260 265 Phe His Arg Ser Gly Ser Pro Thr Val Pro Ile Asn 275

<210> 10

<211> 510

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone Number: 940589

<400> 10

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 Lys
 Ala
 Asp
 Ile
 Lys
 Ile
 Trp
 Ile
 Leu
 Thr
 Gly
 Asp
 Lys
 Gln
 15

 Glu
 Thr
 Ala
 Ile
 Asn
 Ile
 Gly
 His
 Ser
 Cys
 Lys
 Leu
 Lys
 Lys
 Lys

 Asn
 Met
 Gly
 Met
 Ile
 Val
 Ile
 Asn
 Glu
 Gly
 Ser
 Leu
 Asp
 Ser
 Phe

 Ser
 Asn
 Thr
 Gln
 Asn
 Ser
 Arg
 Lys
 Glu
 Ala
 Val
 Leu
 Leu
 Ala
 Lys

 Ser
 Asn
 Thr
 Glu
 Asn
 Ile
 Val
 Ala
 Phe
 Lys
 Glu
 Ser
 Phe
 Glu
 Ala

 Met
 Lys
 His
 Pro
 Asn
 Ile
 Val
 Ala
 Phe
 Lys
 Glu
 Ser
 Phe
 Glu
 Ala

 Glu
 Gly
 His
 Leu
 Tyr
 Lys
 Met
 Glu
 Tyr
 Cy

Leu	Met	Gln	Lys	Ile 95	Lys	Gln	Gln	Lys	Gly 100	Lys	Leu	Phe	Pro	Glu 105
Asp	Met	Ile	Leu	Asn 110	Trp	Phe	Thr	Gln	Met 115	Cys	Leu	Gly	Val	Asn 120
His	Ile	His	Lys	Lys 125	Arg	Val	Leu	His	Arg 130	Asp	Ile	Lys	Ser	Lys 135
Asn	Ile	Phe	Leu	Thr 140	Gln	Asn	Gly	Lys	Val 145	Lys	Leu	Gly	Asp	Phe 150
Gly	Ser	Ala	Arg	Leu 155	Leu	Ser	Asn	Pro	Met 160	Ala	Phe	Ala	Cys	Thr 165
Tyr	Val	Gly	Thr	Pro 170	Tyr	Tyr	Val	Pro	Pro 175	Glu	Ile	Trp	Glu	Asn 180
Leu	Pro	Tyr	Asn	Asn 185	Lys	Ser	Asp	Ile	Trp 190	Ser	Leu	Gly	Cys	Ile 195
	•	Glu		200			-		205					210
		Asn		215					220	_				225
		Ser		230		_			235				-	240
		Lys		245					250					255
		Arg		260					265					270
		Ile		275					280					285
		Ser		290					295					300
		Arg		305					310					315
		Gln	_	320	-	_			325					330
		Asn		335					340	_			_	345
		Gly		350					355	_				360
		His		365					370					375
		Ala		380					385					390
		Asp		395					400					405
				410					415					Leu 420
				425					430					Tyr 435
				440					445					Leu 450
				455					460					Asp 465
ser	vai	тте	Leu	470	Pro	GIU	Arg	ren	G1u 475	rro	GIY	ьeu	Asp	Glu 480
(17.	n	mt-	D		~ 1	G1	~1	n	7	70 -	D	26 -	m-	T7-7
				Phe 485					490			_	_	Val 495 Arg

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<211> 248
<212> PRT
<213> Homo sapiens
<220>
<221> misc feature
<223> Incyte Clone Number: 304421
<400> 11
Met Ala Glu Thr Ser Leu Pro Glu Leu Gly Gly Glu Asp Lys Ala
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Thr Pro Cys Pro Ser Ile Leu Glu Leu Glu Glu Leu Leu Arg Ala
                 20
                                     25
Gly Lys Ser Ser Cys Ser Arg Val Asp Glu Val Trp Pro Asn Leu
                 35
Phe Ile Gly Asp Ala Met Asp Ser Leu Gln Lys Gln Asp Leu Arg
Arg Pro Lys Ile His Gly Ala Val Gln Ala Ser Pro Tyr Gln Pro
Pro Thr Leu Ala Ser Leu Gln Arg Leu Leu Trp Val Arg Gln Ala
Ala Thr Leu Asn His Ile Asp Glu Val Trp Pro Ser Leu Phe Leu
                                    100
Gly Asp Ala Tyr Ala Ala Arg Asp Lys Ser Lys Leu Ile Gln Leu
                110
                                    115
Gly Ile Thr His Val Val Asn Ala Ala Ala Gly Lys Phe Gln Val
                125
                                    130
Asp Thr Gly Ala Lys Phe Tyr Arg Gly Met Ser Leu Glu Tyr Tyr
                140
                                    145
Gly Ile Glu Ala Asp Asp Asn Pro Phe Phe Asp Leu Ser Val Tyr
                                    160
Phe Leu Pro Val Ala Arg Tyr Ile Arg Ala Ala Leu Ser Val Pro
                170
                                    175
Gln Gly Arg Val Leu Val His Cys Ala Met Gly Val Ser Arg Ser
                185
                                    190
Ala Thr Leu Val Leu Ala Phe Leu Met Ile Tyr Glu Asn Met Thr
                200
                                    205
Leu Val Glu Ala Ile Gln Thr Val Gln Ala His Arg Asn Ile Cys
                215
                                    220
Pro Asn Ser Gly Phe Leu Arg Gln Leu Gln Val Leu Asp Asn Arg
                230
                                    235
Leu Gly Arg Glu Thr Gly Arg Phe
                245
<210> 12
<211> 810
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13/64

<212> PRT

<220>

<213> Homo sapiens

<221> misc_feature

<223> Incyte Clone Number: 1213802

<210> 11

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		Asn		35					40					45
Phe	Arg	Gln	Val	Cys 50	Arg	Phe	Arg	His	Met 55	Glu	Ile	Asp	Lys	Lys 60
Arg	Ser	Glu	Ile	Pro 65	Cys	Tyr	Trp	Glu	Asn 70	Gln	Pro	Thr	Gly	Cys 75
		Leu		80					85				_	90
		Leu		95					100					105
		Ser		110					115					120
		Asn		125					130					135
		Val		140					145					150
		Pro		155					160					165
		Asp		170					175					180
		Gln		185					190					195
		Arg		200					205					210
		Gly		215					220					225
		Lys		230					235					240
		Leu		245					250					255
		Arg		260					265					270
		Glu		275					280					285
		Lys		290					295					300
		Leu		305					310					315
		Ile		320					325					330
		Glu		335					340					345
		Asp		350					355					360
		Glu		365					370					375
		Thr		380					385					390
		Ser		395					400					405
Phe	Ser	Glu	Val	Leu	Ala	Glu	Lys	Lys	His	Arg	Gln	Gln	Glu	Ala

				410					415					420
Glu	Arg	Gln	Lys	Ser 425	Lys	Lys	Asp	Thr	Thr 430	Cys	Ile	Lys	Leu	Lys 435
Ile	Asp	Ser	Glu	Ile 440	Lys	Lys	Thr	Val	Val 445	Leu	Pro	Pro	Ile	Val 450
Ala	Ser	Arg	Gly	Gln 455	Ser	Glu	Glu	Pro	Ala 460	Gly	Lys	Thr	Lys	
Met	Gln	Glu	Val		Ile	Lys	Thr	Leu		Glu	Ile	Lys	Leu	
Lys	Ala	Leu	Arg		Gln	Gln	Ser	Ser	-	Ser	Ser	Thr	Ser	
Pro	Ser	Gln	His		Ala	Thr	Pro	Gly		Arg	Arg	Leu	Leu	
Ile	Thr	Lys	Arg		Gly	Met	Lys	Glu		Lys	Asn	Leu	Gln	
Gly	Asn	Glu	Val		Ser	Gln	Ser	Ser	Ile	Arg	Thr	Glu	Ala	Lys
Glu	Ala	Ser	Gly		Thr	Thr	Gly	Val		Ile	Thr	Lys	Ile	
Val	Lys	Arg	Cys		Thr	Met	Arg	Glu		His	Met	Gln	Lys	
Gln	Glu	Arg	Glu		Ser	Val	Leu	Thr		Leu	Arg	Gly	Asp	
Ala	Ser	Cys	Asn		Gln	Val	Ala	Glu		Pro	Val	Leu	Thr	
Val	Pro	Gly	Ile	Thr	Arg	His	Leu	Thr		Arg	Leu	Pro	Thr	
Ser	Ser	Gln	Lys		Glu	Val	Glu	Thr		Gly	Ile	Gly	Asp	
Leu	Leu	Asn	Val		Cys	Ala	Ala	Gln		Leu	Glu	Lys	Arg	
Lys	Ala	Lys	Pro		Val	Asn	Val	Lys		Ser	Val	Val	Lys	
Val	Ser	Ser	Pro		Leu	Ala	Pro	Lys		Lys	Ala	Val	Glu	
His	Ala	Ala	Val		Ala	Ala	Val	Lys		Leu	Ser	Ser	Ser	
Val	Leu	Gln	Glu		Pro	Ala	Lys	Lys		Ala	Val	Ala	Val	
Pro	Leu	Val	Ser		Asp	Lys	Ser	Val		Val	Pro	Glu	Ala	
Asn	Pro	Arg	Asp		Leu	Val	Leu	Pro		Thr	Gln	Ser	Ser	
Asp	Ser	Ser	Pro		Glu	Val	Ser	Gly		Ser	Ser	Ser	Gln	735 Met
Ser	Met	Lys	Thr		Arg	Leu	Ser	Ser	745 Ala	Ser	Thr	Gly	Lys	750 Pro
Pro	Leu	Ser	Val		Asp	Asp	Phe	Glu		Leu	Ile	Trp	Glu	765 Ile
Ser	Gly	Gly	Lys	770 Leu	Glu	Ala	Glu	Ile	775 Asp	Leu	Asp	Pro	Gly	780 Lys
Asp	Glu	Asp	Asp	785 Leu	Leu	Leu	Glu	Leu	790 Ser	Glu	Met	Ile	Asp	795 Ser
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Gly Gly Ser Lys His Thr Met Asn Asp His Leu His Val Gly Ser
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His Ala His Gly Gln Ile Gln Val Arg Gln Leu Phe Glu Asp Asn
Ser Asn Lys Arg Thr Val Leu Thr Thr Gln Pro Asn Gly Leu Thr
                                     55
Thr Val Gly Lys Thr Gly Leu Pro Val Val Pro Glu Arg Gln Leu
                 65
                                     70
Asp Ser Ile His Arg Arg Gln Gly Ser Ser Thr Ser Leu Lys Ser
                 80
                                     85
Met Glu Gly Met Gly Lys Val Lys Ala Thr Pro Met Thr Pro Glu
                                    100
Gln Ala Met Lys Gln Tyr Met Gln Lys Leu Thr Ala Phe Glu His
                110
                                    115
His Glu Ile Phe Ser Tyr Pro Glu Ile Tyr Phe Leu Gly Leu Asn
                125
                                    130
Ala Lys Lys Arg Gln Gly Met Thr Gly Gly Pro Asn Asn Gly Gly
                140
                                    145
Tyr Asp Asp Gln Gly Ser Tyr Val Gln Val Pro His Asp His
                                    160
Val Ala Tyr Arg Tyr Glu Val Leu Lys Val Ile Gly Lys Gly Ser
                170
Phe Gly Gln Val Val Lys Ala Tyr Asp His Lys Val His Gln His
                                    190
Val Ala Leu Lys Met Val Arg Asn Glu Lys Arg Phe His Arg Gln
Ala Ala Glu Glu Ile Arg Ile Leu Glu His Leu Arg Lys Gln Asp
                                    220
Lys Asp Asn Thr Met Asn Val Ile His Met Leu Glu Asn Phe Thr
                230
                                    235
Phe Arg Asn His Ile Cys Met Thr Phe Glu Leu Leu Ser Met Asn
                245
                                    250
Leu Tyr Glu Leu Ile Lys Lys Asn Lys Phe Gln Gly Phe Ser Leu
                260
                                    265
Pro Leu Val Arg Lys Phe Ala His Ser Ile Leu Gln Cys Leu Asp
                275
                                    280
Ala Leu His Lys Asn Arg Ile Ile His Cys Asp Leu Lys Pro Glu
                290
                                    295
Asn Ile Leu Leu Lys Gln Gln Gly Arg Ser Gly Ile Lys Val Ile
                305
                                    310
Asp Phe Gly Ser Ser Cys Tyr Glu His Gln Arg Val Tyr Thr Tyr
                320
                                     325
Ile Gln Ser Arg Phe Tyr Arg Ala Pro Glu Val Ile Leu Gly Ala
                335
                                    340
Arg Tyr Gly Met Pro Ile Asp Met Trp Ser Leu Gly Cys Ile Leu
```

				350)				355					
Ala	Glu	Leu	Leu	Thr	Glv	TV1	Pro	Lau	200	Deed		~ 1	_	360 Glu
				365	;	- / -		, nen	370	PEC	GIY	GIU	ı Asp	
Gly	' Asp	Gln	Leu	Ala	Cvs	Met	Tle	Glu	3 / U	Tou	<i>α</i> 1		_	375 Ser
				380				014	385		GIY	Met	Pro	
Gln	Lys	Leu	Leu	Asp	Ala	Ser	Lvs	Ara	Δla	Lvc	λαπ	Dha	77-7	390 Ser
				395					400					400
Ser	Lys	Gly	Tyr	Pro	Arg	Tyr	Cvs	Thr	Val	Thr	Thr	T OV	Com	405
				410					415					400
Gly	Ser	Val	Val	Leu	Asn	Gly	Gly	Arg	Ser	Ara	Ara	Glv	Larc	420
				425					430					425
Arg	Gly	Pro	Pro	Glu	Ser	Arg	Glu	Trp	Glv	Asn	Ala	Len	Lvc	G] 11
				440					445					450
Cys	Asp	Asp	Pro	Leu	Phe	Leu	Asp	Phe	Leu	Lvs	Gln	Cvs	Leu	G111
				455					460					465
Trp	Asp	Pro	Ala	Val	Arg	Met	Thr	Pro	Gly	Gln	Ala	Leu	Ara	His
				4 / 0					475					400
Pro	Trp	Leu	Arg	Arg	Arg	Leu	Pro	Lys	Pro	Pro	Thr	Glv	Glu	Lvs
				485					490					405
rnr	ser	Val	Lys	Arg	Ile	Thr	Glu	Ser	Thr	Gly	Ala	Ile	Thr	Ser
				500					505					E 1 0
тте	ser	Lys	Leu	Pro	Pro	Pro	Ser	Ser	Ser	Ala	Ser	Lys	Leu	Arq
		•		212					520					
1111	ASII	Leu	Ala	Gln	Met	Thr	Asp	Ala	Asn	Gly	Asn	Ile	Gln	Gln
				230					535					540
AL Y	THE	Val			Lys	Leu	Val	Ser						
				545										

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<212> PRT

<213> Homo sapiens

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	125				130					135
Lys Ala Met	Glu Ser	Lys I	Lys Thr	Tyr	Glu	${\tt Gln}$	Lys	Cys	Arg	Asp
	140				145					150
Ala Asp Asp			Ala Phe	Glu	Arg	Ile	Ser	Ala	Asn	Gly
	155				160					165
His Gln Lys			Lys Ser	Gln		Lys	Ala	Arg	Gln	Cys
	170				175					180
Lys Asp Ser			Ala Glu	Arg		Tyr	Arg	Gln	Ser	
Ala Cla Lou	185		\ 3.1-	a n	190	~ 1	~1	~3		195
Ala Gln Leu	200	Val A	arg Ala	GIU		GIU	GIn	GIU	HIS	
Thr Thr Cys		Phe C	Iln Iou	C1 5	205	Dha	3	7	T	210
imi imi cys	215	rne e	orn bed	GIII	220	Pne	Asp	Arg	ьец	225
Ile Leu Arg		Len T	rro Val	Hie		Δen	Gln	T.011	Sar	
	230		ip var	******	235	7.511	GIII	пец	Der	240
Gln Cys Val		Asp G	3lu Leu	Tvr		Glu	Val	Ara	Leu	
-	245	-		•	250			5		255
Leu Glu Gly	Cys Ser	Ile A	Asp Ala	Asp	Ile	Asp	Ser	Phe	Ile	
	260			_	265	-				270
Ala Lys Ser	Thr Gly	Thr G	Slu Pro	Pro	Ala	Pro	Val	Pro	Tyr	Gln
	275				280					285
Asn Tyr Tyr	Asp Arg	Glu V	al Thr	Pro	Leu	Thr	Ser	Ser	Pro	Gly
	290				295					300
Ile Gln Pro		Gly M	Met Ile	Lys		Phe	Ser	Gly	Leu	
71 - Gl G	305		n) ~	_	310					315
His Gly Ser		Thr T	hr Ser	Leu		Ala	Ser	Ala	Ala	
ም ኮ ም ሮቪ፣ ሞኮም	320	Dwo III	Thus Dags	a a	325		~ 1	~ 1	**. 7	330
Thr Glu Thr	335	PIOI	ini Pro	GIU	Arg 340	Asn	GIU	GIY	vaı	
Thr Ala Ile		Gln G	בוד יוני	Gln		λαπ	Dro	- ות	802	345
	350	0111	JIW IIG	GIII	355	ASII	FIO	на	Ser	360
Ala Gln Glu		Ala L	eu Tvr	Asp		Thr	Δla	Gln	Asn	
	365				370			0111		375
Asp Glu Leu	Asp Leu	Ser A	la Gly	Asp	Ile	Leu	Glu	Val	Ile	
	380		-	•	385					390
Glu Gly Glu	Asp Gly	Trp T	rp Thr	Val	Glu	Arg	Asn	Gly	Gln	Arg
	395				400			_		405
Gly Phe Val	Pro Gly	Ser T	Tyr Leu	Glu	Lys	Leu				
	410				415					
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Val	Leu	Val	Glu	Ala 50	Thr	Val	Lys	Leu	Asp 55	Glu	Leu	Val	Lys	Lys 60
Ile	Gly	Lys	Ala		Glu	Asp	Ser	Lys	Pro	Tyr	Trp	Glu	Ala	
Arg	Val	Ala	Arg	Gln 80	Ala	Gln	Leu	Glu	Ala 85	Gln	Lys	Ala	Thr	Gln 90
Asp	Phe	Gln	Arg	Ala 95	Thr	Glu	Val	Leu	Arg 100	Ala	Ala	Lys	Glu	Thr 105
Ile	Ser	Leu	Ala	Glu 110	Gln	Arg	Leu	Leu	Glu 115	Asp	Asp	Lys	Arg	Gln 120
Phe	Asp	Ser	Ala	Trp 125	Gln	Glu	Met	Leu	Asn 130	His	Ala	Thr	Gln	Arg 135
Val	Met	Glu	Ala	Glu 140	Gln	Thr	Lys	Thr	Arg 145	Ser	Glu	Leu	Val	His 150
Lys	Glu	Thr	Ala	Ala 155	Arg	Tyr	Asn	Ala	Ala 160	Met	Gly	Arg	Met	Arg 165
Gln	Leu	Glu	Lys	Lys 170	Leu	Lys	Arg	Ala	11e 175	Asn	Lys	Ser	Lys	Pro 180
_	Phe			185		_	_	_	190					195
-	Lys			200	-				205					210
_	Glu	_	-	215			-		220					225
	Ile			230	_	_			235		-		_	240
	Gly		_	245					250					255
	Gly			260			_		265					270
	Phe		-	275		-			280				_	285
	Glu			290					295		_			300
	Ser			305	_				310			_		315
	Leu	-		320					325				-	330
	Phe			335	_		_		340	-		_		345
	Pro			350					355					360
	Asn			365					370					375
	Ser			380	_				385					390
	Pro			395					400					405
	Gln			410	Gly	Arg	Asp	Gly	Ile 415	Ile	Ala	Asp	Ile	Lys 420
Met	Val	Gln	Ile	Gly 425										

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Val Pro Gly Glu Ser Thr Leu Arg Arg Asp Phe Leu Arg Leu Gln

				350					255					360
Gln	Glu	Asn	Lvs	Glu	Ara	Ser	Glu	Δla	355 Leu	Δτα	Ara	Gln	Gln	
			-,, -	365			Ozu		370	9	111.9	0111	0111	375
Leu	Gln	Glu	Gln	Gln	Leu	Arg	Glu	Gln		Glu	Tyr	Lys	Arq	
				380					385		-	-		390
Leu	Leu	Ala	Glu	Arg	Gln	Lys	Arg	Ile	Glu	Gln	Gln	Lys	Glu	Gln
				395					400					405
Arg	Arg	Arg	Leu	Glu	Glu	Gln	Gln	Arg		Glu	Arg	Glu	Ala	
7 ~~	Cln	Cln	<i>α</i> 1	410	C1.	<i>~</i> 1~	7	3	415	a 1	a)	01	21	420
Arg	GIII	GIII	Gru	Arg 425	GIU	GIII	Arg	Arg	430	GIU	GIN	GIU	GIU	ьуs 435
Arq	Arq	Leu	Glu	Glu	Leu	Glu	Arg	Ara		Lvs	Glu	Glu	Glu	
	,			440			3	5	445	-1-				450
Arg	Arg	Arg	Ala	Glu	Glu	Glu	Lys	Arg	Arg	Val	Glu	Arg	Glu	Gln
				455					460					465
Glu	Tyr	Ile	Arg	Arg	Gln	Leu	Glu	Glu		Gln	Arg	His	Leu	
	_		~3	470	_	_			475				_	480
Val	Leu	Gin	GIn	Gln 485	Leu	Leu	GIn	Glu		Ala	Met	Leu	Leu	His 495
Asp	His	Ara	Ara	Pro	His	Pro	Gln	Hie	490 Ser	Gln	Gln	Dro	Pro	
пор		9	•••	500	******	110	0111	111.5	505	GIII	GIII	110	110	510
Pro	Gln	Gln	Glu	Arg	Ser	Lys	Pro	Ser		His	Ala	Pro	Glu	
				515		-			520					525
Lys	Ala	His	Tyr	Glu	Pro	Ala	Asp	Arg	Ala	Arg	Glu	Val	Pro	Val
				530					535					540
Arg	Thr	Thr	Ser	Arg	Ser	Pro	Val	Leu		Arg	Arg	Asp	Ser	
Lou	Cln	C111	805	545	C1.5	C1 -	7		550	21-	01	a 1	N ~~~	555
Leu	GIII	GIY	ser	Gly 560	GIII	GIII	ASII	ser	565	Ala	GIA	GIII	Arg	570
Ser	Thr	Ser	Ile	Glu	Pro	Arq	Leu	Leu		Glu	Arg	Val	Glu	
				575		5			580		3			585
Leu	Val	Pro	Arg	Pro	Gly	Ser	Gly	Ser	Ser	Ser	Gly	Ser	Ser	Asn
				590					595					600
Ser	Gly	Ser	Gln	Pro	Gly	Ser	His	Pro	_	Ser	Gln	Ser	Gly	
C111	C1,,	7 ~~	Dho	605	17-7	N	Com	C	610	7		<i>α</i> 3	C1	615
Gry	GIL	Arg	FIIE	Arg 620	val	Arg	per	ser	625	цуѕ	ser	GIU	GIY	630
Pro	Ser	Gln	Arq	Leu	Glu	Asn	Ala	Val		Lvs	Pro	Glu	asa	
			,	635					640	-1-				645
Lys	Glu	Val	Phe	Arg	Pro	Leu	Lys	Pro	Ala	Asp	Leu	Thr	Ala	Leu
				650					655					660
Ala	Lys	Glu	Leu	Arg	Ala	Val	Glu	Asp		Arg	Pro	Pro	His	
77a 7	mh.∽	λ a.s.	TT	665	Com	C ~ ~	C ~	a 1	670	0	G1	m1	m b	675
vai	1111	Азр	TYL	Ser 680	ser	ser	ser	GIU	685	ser	GIY	THE	Inr	690
Glu	Glu	asa	Asp	Asp	Val	Glu	Gln	Glu		Ala	Asp	Glu	Ser	
		•	-	695					700		F			705
Ser	Gly	Pro	Glu	Asp	Thr	Arg	Ala	Ala	Ser	Ser	Leu	Asn	Leu	Ser
				710					715					720
Asn	Gly	Glu	Thr	Glu	Ser	Val	Lys	Thr		Ile	Val	His	Asp	
77. 7	a3		<i>a</i> 3	725			>	_	730			~ -	1	735
val	GLu	ser	GLu	Pro	Ala	Met	Thr	Pro		Lys	Glu	Gly	Thr	
IJe	Val	Arg	Gln	740 Thr	Gln	Ser	Ala	Ser	745 Ser	Thr	Len	Gln	Lve	750 His
		3		755	5111	001	111 a	Der	760	* 111	Leu	4111	Lys	765
Lys	Ser	Ser	Ser	Ser	Phe	Thr	Pro	Phe		Asp	Pro	Arg	Leu	
										-				

				770										700
Cln	Tlo	Cox	Dwo	770	Cor	C1**	Thr	mb x	775	mh =	Com	1703	ו בעד	780
Gili	116	Ser	PIO	785	ser	GTY	1111	1111	790	TILL	ser	vai	Val	795
Phe	Ser	Cys	Asn		Met	Δτα	Pro	Glu		Tle	Δτα	Gln	Δen	
1110	DCI	Cys	7,55	800	1100	9	110	OIU	805	110	Arg	0111	АЗР	810
Thr	Ara	Lys	Glv		Val	Val	Asn	Val		Pro	Thr	Asn	Thr	
	5	-1-	1	815					820					825
Pro	Gln	Ser	Asp		Pro	Glu	Ile	Arg		Tvr	Lvs	Lvs	Arq	
			-	830				•	835	•	•	•	_	840
Asn	Ser	Glu	Ile	Leu	Cys	Ala	Ala	Leu	Trp	Gly	Val	Asn	Leu	Leu
				845					850					855
Val	Gly	Thr	Glu	Ser	Gly	Leu	Met	Leu	Leu	Asp	Arg	Ser	Gly	Gln
				860					865					870
Gly	Lys	Val	Tyr		Leu	Ile	Asn	Arg	_	Arg	Phe	Gln	Gln	
_		_		875	_	_		_	880			_		885
Asp	Val	Leu	GIu		Leu	Asn	Val	Leu		Thr	Ile	Ser	GIY	_
Taro	Λαn	Lys	T OU	890	T/a l	Ф. г.	T-1	T 011	895 Sox	There	Lou	7 ~~	ħ a n	900
nys	Asp	цуѕ	пеп	905	val	TYL	TYL	пеп	910	пр	Leu	Arg	ASII	915
Ile	Leu	His	Asn		Pro	Glu	Val	Glu		Lvs	Gln	Glv	Tro	
				920					925	_,_	0	4-1	-	930
Thr	Val	Gly	Asp	Leu	Glu	Gly	Cys	Val	His	Tyr	Lys	Val	Val	Lys
				935					940	_	_			945
Tyr	Glu	Arg	Ile	Lys	Phe	Leu	Val	Ile	Ala	Leu	Lys	Ser	Ser	Val
				950					955					960
Glu	Val	Tyr	Ala		Ala	Pro	Lys	Pro	_	His	Lys	Phe	Met	
n1	. _	a	m1	965	63	.	**- 1		970	a .	_		~1	975
Pne	ьуs	Ser	Pne	980	GIU	Leu	vai	HIS	985	ser	Cys	Ата	GIY	990
His	Ala	Val	Agn		Asp	Ser	Glv	Ser		Tur	Asn	Tle	ጥህዮ	
			p	995	шр	501	0.1		1000	- 7 -	шър		-	1005
Pro	Thr	His	Ile	Gln	Cys	Ser	Ile			His	Ala	Ile		
			:	1010					1015					1020
Leu	Pro	Asn	Thr	Asp	Gly	Met	Glu	Leu	Leu	Val	Cys	Tyr	Glu	Asp
				1025					1030					1035
Glu	Gly	Val			Asn	Thr	Tyr	_	_	Ile	Thr	Lys	_	
**- 7	.	~ 1 -		1040	a 1		D	-	1045					1050
vai	Leu	Gln			GIU	met	Pro			vaı	Ala	Tyr		
Ser	Δen	Gln		1055 Met	Glv	רגייניים	Glv		1060	Δla	Tla	Glu		1065 Ara
501		0111		1070	017				1075		110	014		1080
Ser	Val	Glu			His	Leu	Asp				Met	His		Arg
				1085			-		1090					1095
Ala	Gln	Arg	Leu	Lys	Phe	Leu	Cys	Glu	Arg	Asn	Asp	Lys	Val	Phe
				1100					1105					1110
Phe	Ala	Ser			Ser	Gly	Gly			Gln	Val	Tyr		
	_			1115	_	_	_		1120					1125
Thr	Leu	Gly			Ser	Leu	Leu		_					
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<213> Homo sapiens

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Lys His Ile Asn Ile Ser Phe His Arg Phe Pro Leu Asp Pro Lys
                 20
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Arg Arg Lys Glu Trp Val Arg Leu Val Arg Arg Lys Asn Phe Val
                 35
                                     40
Pro Gly Lys His Thr Phe Leu Cys Ser Lys His Phe Glu Ala Ser
                 50
Cys Phe Asp Leu Thr Gly Gln Thr Arg Arg Leu Lys Met Asp Ala
                 65
                                     70
Val Pro Thr Ile Phe Asp Phe Cys Thr His Ile Lys Ser Met Lys
                 80
                                     85
Leu Lys Ser Arg Asn Leu Leu Lys Lys Asn Asn Ser Cys Ser Pro
                                    100
Ala Gly Pro Ser Asn Leu Lys Ser Asn Ile Ser Ser Gln Gln Val
                                    115
Leu Leu Glu His Ser Tyr Ala Phe Arg Asn Pro Met Glu Ala Lys
                                    130
Lys Arg Ile Ile Lys Leu Glu Lys Glu Ile Ala Ser Leu Arg Arg
Lys Met Lys Thr Cys Leu Gln Lys Glu Arg Arg Ala Thr Arg Arg
                                    160
Trp Ile Lys Ala Thr Cys Leu Val Lys Asn Leu Glu Ala Asn Ser
                170
                                    175
Val Leu Pro Lys Gly Thr Ser Glu His Met Leu Pro Thr Ala Leu
                185
                                    190
Ser Ser Leu Pro Leu Glu Asp Phe Lys Ile Leu Glu Gln Asp Gln
                200
                                    205
Gln Asp Lys Thr Leu Leu Ser Leu Asn Leu Lys Gln Thr Lys Ser
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                                    220
Thr Phe Ile
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<213> Homo sapiens

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<223> Incyte Clone Number: 1384286

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 Thr
 Thr
 Val
 Thr
 Cys
 Thr
 Arg
 Phe
 Thr
 Asp
 Glu
 Tyr
 Gln

 Leu
 Tyr
 Glu
 Asp
 Ile
 Gly
 Lys
 Gly
 Ala
 Phe
 Ser
 Val
 Val
 Arg
 Arg

 Cys
 Val
 Lys
 Leu
 Cys
 Thr
 Gly
 His
 Glu
 Tyr
 Ala
 Ala
 Lys
 Ile
 Ile

 Asn
 Thr
 Lys
 Leu
 Ser
 Ala
 Arg
 Asp
 His
 Gln
 Lys
 Leu
 Glu
 Arg



				50					55					60
Glu	Ala	Arg	Ile	Cys 65	Arg	Leu	Leu	Lys	His 70	Ser	Asn	Ile	Val	Arg 75
Leu	His	Asp	Ser	Ile 80	Ser	Glu	Glu	Gly	Phe 85	His	Tyr	Leu	Val	Phe 90
Asp	Leu	Val	Thr	Gly 95	Gly	Glu	Leu	Phe	Glu 100	Asp	Ile	Val	Ala	Arg 105
Glu	Tyr	Tyr	Ser	Glu 110	Ala	Asp	Ala	Ser	His 115	Cys	Ile	Gln	Gln	Ile 120
Leu	Glu	Ala	Val	Leu 125	His	Cys	His	Gln	Met 130	Gly	Val	Val	His	Arg 135
Asp	Leu	Lys	Pro	Glu 140	Asn	Leu	Leu	Leu	Ala 145	Ser	Lys	Cys	Lys	Gly 150
Ala	Ala	Val	Lys	Leu 155	Ala	Asp	Phe	Gly	Leu 160	Ala	Ile	Glu	Val	Gln 165
Gly	Asp	Gln	Gln	Ala 170	Trp	Phe	Gly	Phe	Ala 175	Gly	Thr	Pro	Gly	Tyr 180
Leu	Ser	Pro	Glu	Val 185	Leu	Arg	Lys	Glu	Ala 190	Tyr	Gly	Lys	Pro	Val 195
Asp	Ile	Trp	Ala	Cys 200	Gly	Val	Ile	Leu	Tyr 205	Ile	Leu	Leu	Val	Gly 210
Tyr	Pro	Pro	Phe	Trp 215	Asp	Glu	Asp	Gln	His 220	Lys	Leu	Tyr	Gln	Gln 225
Ile	Lys	Ala	Gly	Ala 230	Tyr	Asp	Phe	Pro	Ser 235	Pro	Glu	Trp	Asp	Thr 240
Val	Thr	Pro	Glu	Ala 245	Lys	Asn	Leu	Ile	Asn 250	Gln	Met	Leu	Thr	Ile 255
Asn	Pro	Ala	Lys	Arg 260	Ile	Thr	Ala	His	Glu 265	Ala	Leu	Lys	His	Pro 270
Trp	Val	Cys	Gln	Arg 275	Ser	Thr	Val	Ala	Ser 280	Met	Met	His	Arg	Gln 285
			Glu	290		_	_		295		_	_	-	300
Lys	Gly	Ala	Ile	Leu 305	Thr	Thr	Met	Leu	Ala 310	Thr	Arg	Asn	Phe	Ser 315
			Ser	320			_	_	325	_	-		_	330
His	Thr	Asn	Ser	Thr 335	Lys	Asn	Ser	Ala	Ala 340	Ala	Thr	Ser	Pro	Lys 345
_			Pro	350					355		_			360
				365		-		•	370	J	-			Ile 375
			Thr	380					385					390
Phe	Glu	Ala	Tyr	Ala 395	Lys	Ile	Cys	Asp	Pro 400	Gly	Leu	Thr	Ser	Phe 405
			Ala	410					415	_				420
		_	Phe	425					430					435
			Ile	440					445			_		450
Ala	Ala	Cys	Ile	Ala 455	Tyr	Ile	Arg	Leu	Thr 460	Gln	Tyr	Ile	Asp	Gly 465
Gln	Gly	Arg	Pro	Arg	Thr	Ser	Gln	Ser	Glu	Glu	Thr	Arg	Val	Trp

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      His Arg Arg Arg
      Asp Gly Lys Trp Gln Asn 490
      Val His Phe His Cys Ser 485
      485
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275
                                    280
Ile Leu Leu Ser Glu Pro Glu Asn Ala Asp Ser Leu Met Leu
Val Asp Phe Glu Tyr Ser Ser Tyr Asn Tyr Arg Gly Phe Asp Ile
Gly Asn His Phe Cys Glu Trp Val Tyr Asp Tyr Thr His Glu Glu
Trp Pro Phe Tyr Lys Ala Arg Pro Thr Asp Tyr Pro Thr Gln Glu
                                    340
Gln Gln Leu His Phe Ile Arg His Tyr Leu Ala Glu Ala Lys Lys
                350
                                    355
Gly Glu Thr Leu Ser Gln Glu Glu Gln Arg Lys Leu Glu Glu Asp
                365
                                    370
Leu Leu Val Glu Val Ser Arg Tyr Ala Leu Ala Ser His Phe Phe
                380
                                    385
Trp Gly Leu Trp Ser Ile Leu Gln Ala Ser Met Ser Thr Ile Glu
                395
                                    400
Phe Gly Tyr Leu Asp Tyr Ala Gln Ser Arg Phe Gln Phe Tyr Phe
                410
                                    415
                                                        420
Gln Gln Lys Gly Gln Leu Thr Ser Val His Ser Ser Ser
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<211> 527

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone Number: 2098635

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170 175	180
Arg Val Phe Arg Glu Leu Lys Met Leu Cys Phe Phe Lys H	
185 190 Asn Val Leu Ser Ala Leu Asp Ile Leu Gln Pro Pro His I	195 Le Asp
200 205	210
Tyr Phe Glu Glu Ile Tyr Val Val Thr Glu Leu Met Gln S	
215 220	225
Leu His Lys Ile Ile Val Ser Pro Gln Pro Leu Ser Ser A	-
230 235 Val Lys Val Phe Leu Tyr Gln Ile Leu Arg Gly Leu Lys T	240
245 250	255
His Ser Ala Gly Ile Leu His Arg Asp Ile Lys Pro Gly A	
260 265	270
Leu Val Asn Ser Asn Cys Val Leu Lys Ile Cys Asp Phe G	-
275 280	285
Ala Arg Val Glu Glu Leu Asp Glu Ser Arg His Met Thr G 290 295	
Val Val Thr Gln Tyr Tyr Arg Ala Pro Glu Ile Leu Met G	300 v Ser
305 310	315
Arg His Tyr Ser Asn Ala Ile Asp Ile Trp Ser Val Gly C	
320 325	330
Phe Ala Glu Leu Leu Gly Arg Arg Ile Leu Phe Gln Ala G	
335 340	345
Pro Ile Gln Gln Leu Asp Leu Ile Thr Asp Leu Leu Gly T 350 355	360
Ser Leu Glu Ala Met Arg Thr Ala Cys Glu Gly Ala Lys A	
365 370	375
Ile Leu Arg Gly Pro His Lys Gln Pro Ser Leu Pro Val L	eu Tyr
385	390
Thr Leu Ser Ser Gln Ala Thr His Glu Ala Val His Leu L	-
395 400 Arg Met Leu Val Phe Asp Pro Ser Lys Arg Ile Ser Ala L	405
410 415	420
Ala Leu Ala His Pro Tyr Leu Asp Glu Gly Arg Leu Arg T	r His
425 430	435
Thr Cys Met Cys Lys Cys Cys Phe Ser Thr Ser Thr Gly A	•
440 445 Tyr Thr Ser Asp Phe Glu Pro Val Thr Asn Pro Lys Phe A	450
455 460	465
Thr Phe Glu Lys Asn Leu Ser Ser Val Arg Gln Val Lys G	
470 475	480
Ile His Gln Phe Ile Leu Glu Gln Gln Lys Gly Asn Arg V	
485 490	495
Leu Cys Ile Asn Pro Gln Ser Ala Ala Phe Lys Ser Phe I 500 505	le Ser 510
Ser Thr Val Ala Gln Pro Ser Glu Met Pro Pro Ser Pro L	
515 520	525

<210> 21

<211> 322

<212> PRT

<213> Homo sapiens

<220>

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<400> 21 Met Glu Gly Ile Ser Asn Phe Lys Thr Pro Ser Lys Leu Ser Glu Lys Lys Lys Ser Val Leu Cys Ser Thr Pro Thr Ile Asn Ile Pro Ala Ser Pro Phe Met Gln Lys Leu Gly Phe Gly Thr Gly Val Asn Val Tyr Leu Met Lys Arg Ser Pro Arg Gly Leu Ser His Ser Pro 50 Trp Ala Val Lys Lys Ile Asn Pro Ile Cys Asn Asp His Tyr Arg Ser Val Tyr Gln Lys Arg Leu Met Asp Glu Ala Lys Ile Leu Lys 85 Ser Leu His His Pro Asn Ile Val Gly Tyr Arg Ala Phe Thr Glu 95 100 Ala Asn Asp Gly Ser Leu Cys Leu Ala Met Glu Tyr Gly Glu 110 115 Lys Ser Leu Asn Asp Leu Ile Glu Glu Arg Tyr Lys Ala Ser Gln 125 130 Asp Pro Phe Pro Ala Ala Ile Ile Leu Lys Val Ala Leu Asn Met 140 145 Ala Arg Gly Leu Lys Tyr Leu His Gln Glu Lys Lys Leu Leu His 155 160 Gly Asp Ile Lys Ser Ser Asn Val Val Ile Lys Gly Asp Phe Glu 170 175 Thr Ile Lys Ile Cys Asp Val Gly Val Ser Leu Pro Leu Asp Glu 190 Asn Met Thr Val Thr Asp Pro Glu Ala Cys Tyr Ile Gly Thr Glu Pro Trp Lys Pro Lys Glu Ala Val Glu Glu Asn Gly Val Ile Thr 215 Asp Lys Ala Asp Ile Phe Ala Phe Gly Leu Thr Leu Trp Glu Met Met Thr Leu Ser Ile Pro His Ile Asn Leu Ser Asn Asp Asp Asp Asp Glu Asp Lys Thr Phe Asp Glu Ser Asp Phe Asp Asp Glu Ala 260 265 Tyr Tyr Ala Ala Leu Gly Thr Arg Pro Pro Ile Asn Met Glu Glu 275 280 Leu Asp Glu Ser Tyr Gln Lys Val Ile Glu Leu Phe Ser Val Cys 295 Thr Asn Glu Asp Pro Lys Asp Arg Pro Ser Ala Ala His Ile Val 305 310 315 Glu Ala Leu Glu Thr Asp Val 320

<210> 22

<211> 802

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone Number: 2764911

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				395					400					405
Thr	Asn	Val	Ala	Arg 410	Ser	Ala	Met	Met	Lys 415	Asp	Ser	Pro	Phe	Tyr 420
Gln	His	Tyr	Asp	Leu 425	Asp	Leu	Lys	Asp	Lys 430	Pro	Leu	Gly	Glu	Gly 435
Ser	Phe	Ser	Ile	Cys 440	Arg	Lys	Cys	Val	His 445	Lys	Lys	Ser	Asn	Gln 450
Ala	Phe	Ala	Val	Lys 455	Ile	Ile	Ser	Lys	Arg 460	Met	Glu	Ala	Asn	Thr 465
				470					475				Pro	480
Ile	Val	Lys	Leu	His 485	Glu	Val	Phe	His	Asp 490	Gln	Leu	His	Thr	Phe 495
				500			_	_	505				Arg	510
				515					520			_	Ile	525
_	-			530					535		_		Gly	540
		_	_	545	-				550				Asp	555
				560					565		_		Ala	570
				575					580			_	Phe _	585
		_		590					595			-	Tyr	600
				605					610			_	Thr	615
				620					625	_	_		Leu	630
				635				-	640		-	_	Gly	645
				650			_	_	655				Glu	660
	_			665	_				670	_			Lys	675
				680					685	_			Asp	690
				695					700		_		Leu	705
				710				-	715				Phe Asn	720
				725					730					735
				740					745				Thr	750
				755					760				His	765
				770		_	-		775			-	Thr	780
				785		_	ser	ASII	790	PEO	GIU	THE	Leu	795
GIII	rne	Ser	rsb	800	val	MIG								

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<212> PRT
<213> Homo sapiens
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<221> misc_feature
<223> Incyte Clone Number: 3013946
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Leu Tyr Glu Asp Ile Gly Lys Gly Ala Phe Ser Val Val Arg Arg
                 20
                                     25
Cys Val Lys Leu Cys Thr Gly His Glu Tyr Ala Ala Lys Ile Ile
Asn Thr Lys Lys Leu Ser Ala Arg Asp His Gln Lys Leu Glu Arg
                                     55
Glu Ala Arg Ile Cys Arg Leu Leu Lys His Ser Asn Ile Val Arg
                                     70
Leu His Asp Ser Ile Ser Glu Glu Gly Phe His Tyr Leu Val Phe
Asp Leu Val Thr Gly Gly Glu Leu Phe Glu Asp Ile Val Ala Arg
                 95
                                    100
Glu Tyr Tyr Ser Glu Ala Asp Ala Ser His Cys Ile Gln Gln Ile
                                    115
                110
Leu Glu Ala Val Leu His Cys His Gln Met Gly Val Val His Arg
                125
                                    130
Asp Leu Lys Pro Glu Asn Leu Leu Ala Ser Lys Cys Lys Gly
                                    145
Ala Ala Val Lys Leu Ala Asp Phe Gly Leu Ala Ile Glu Val Gln
                155
                                    160
Gly Asp Gln Gln Ala Trp Phe Gly Phe Ala Gly Thr Pro Gly Tyr
                170
                                    175
Leu Ser Pro Glu Val Leu Arg Lys Glu Ala Tyr Gly Lys Pro Val
                                    190
                185
Asp Ile Trp Ala Cys Gly Val Ile Leu Tyr Ile Leu Leu Val Gly
                200
                                    205
Tyr Pro Pro Phe Trp Asp Glu Asp Gln His Lys Leu Tyr Gln Gln
                215
                                    220
Ile Lys Ala Gly Ala Tyr Asp Phe Pro Ser Pro Glu Trp Asp Thr
                230
                                    235
Val Thr Pro Glu Ala Lys Asn Leu Ile Asn Gln Met Leu Thr Ile
                245
                                    250
Asn Pro Ala Lys Arg Ile Thr Ala His Glu Ala Leu Lys His Pro
                                     265
Trp Val Cys Gln Arg Ser Thr Val Ala Ser Met Met His Arg Gln
                                     280
Glu Thr Val Glu Cys Leu Lys Lys Phe Asn Ala Arg Arg Lys Leu
                290
                                     295
Lys Gly Ala Ile Leu Thr Thr Met Leu Ala Thr Arg Asn Phe Ser
Ala Lys Ser Leu Leu Asn Lys Lys Ala Asp Gly Val Lys Pro Gln
                320
                                     325
Thr Asn Ser Thr Lys Asn Ser Ala Ala Ala Thr Ser Pro Lys Gly
                335
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<210> 23

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Thr Leu Pro Pro Ala Ala Leu Glu Pro Gln Thr Thr Val Ile His
                                     355
Asn Pro Val Asp Gly Ile Lys Glu Ser Ser Asp Ser Ala Asn Thr
Thr Ile Glu Asp Glu Asp Ala Lys Ala Pro Arg Val Pro Asp Ile
                380
                                     385
Leu Ser Ser Val Arg Arg Gly Ser Gly Ala Pro Glu Ala Glu Gly
                395
                                     400
Pro Leu Pro Cys Pro Ser Pro Ala Pro Phe Gly Pro Leu Pro Ala
                410
                                     415
Pro Ser Pro Arg Ile Ser Asp Ile Leu Asn Ser Val Arg Arg Gly
                425
                                    430
Ser Gly Thr Pro Glu Ala Glu Gly Pro Leu Ser Ala Gly Pro Pro
                440
                                     445
                                                         450
Pro Cys Leu Ser Pro Ala Leu Leu Gly Pro Leu Ser Ser Pro Ser
                455
                                     460
Pro Arg Ile Ser Asp Ile Leu Asn Ser Val Arg Arg Gly Ser Gly
                470
                                     475
Thr Pro Glu Ala Lys Gly Pro Ser Pro Val Gly Pro Pro Pro Cys
                485
                                     490
Pro Ser Pro Thr Ile Pro Gly Pro Leu Pro Thr Pro Ser Arg Lys
                500
                                     505
Gln Glu Ile Ile Lys Thr Thr Glu Gln Leu Ile Glu Ala Val Asn
                515
                                     520
Asn Gly Asp Phe Glu Ala Tyr Ala Lys Ile Cys Asp Pro Gly Leu
                530
                                     535
Thr Ser Phe Glu Pro Glu Ala Leu Gly Asn Leu Val Glu Gly Met
                                     550
Asp Phe His Arg Phe Tyr Phe Glu Asn Leu Leu Ala Lys Asn Ser
                                     565
Lys Pro Ile His Thr Thr Ile Leu Asn Pro His Val His Val Ile
Gly Glu Asp Ala Ala Cys Ile Ala Tyr Ile Arg Leu Thr Gln Tyr
Ile Asp Gly Gln Gly Arg Pro Arg Thr Ser Gln Ser Glu Glu Thr
                                     610
Arg Val Trp His Arg Arg Asp Gly Lys Trp Gln Asn Val His Phe
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                                     625
His Cys Ser Gly Ala Pro Val Ala Pro Leu Gln
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<211> 588

<212> PRT

<213> Homo sapiens

<220>

<221> misc feature

<223> Incyte Clone Number: 067967

<400> 24

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Pro Gly Ala Gly Leu Pro Pro Gln Gln Arg Arg Leu Gly Asp Gly 20 25 30

Val Tyr Asp Thr Phe Met Met Ile Asp Glu Thr Lys Cys Pro Pro

				35					40					45
Cys	Ser	Asn	Val	Leu 50	Cys	Asn	Pro	Ser	Glu 55	Pro	Pro	Ser	Pro	Arg 60
Arg	Leu	Asn	Met	Thr 65	Thr	Glu	Gln	Phe	Thr 70	Gly	Asp	His	Thr	Gln 75
His	Phe	Leu	Asp	Gly 80	Gly	Glu	Met	Lys	Val 85	Glu	Gln	Leu	Phe	Gln 90
Glu	Phe	Gly	Asn	Arg 95	Lys	Ser	Asn	Thr	Ile 100	Gln	Ser	Asp	Gly	Ile 105
Ser	Asp	Ser	Glu	Lys 110	Cys	Ser	Pro	Thr	Val 115	Ser	Gln	Gly	Lys	Ser 120
Ser	Asp	Cys	Leu	Asn 125	Thr	Val	Lys	Ser	Asn 130	Ser	Ser	Ser	Lys	Ala 135
Pro	Lys	Val	Val	Pro 140	Leu	Thr	Pro	Glu	Gln 145	Ala	Leu	Lys	Gln	Tyr 150
Lys	His	His	Leu	Thr 155	Ala	Tyr	Glu	Lys	Leu 160	Glu	Ile	Ile	Asn	Tyr 165
Pro	Glu	Ile	Tyr	Phe 170	Val	Gly	Pro	Asn	Ala 175	Lys	Lys	Arg	His	Gly 180
		-	-	185			_	-	190	-			Asp	195
				200					205				Tyr	210
Val	Leu	Lys	Ile	Ile 215	Gly	Lys	Gly	Ser	Phe 220	Gly	Gln	Val	Ala	Arg 225
Val	Tyr	Asp	His	Lys 230	Leu	Arg	Gln	Tyr	Val 235	Ala	Leu	Lys	Met	Val 240
			_	245			_		250				Ile	255
Ile	Leu	Glu	His	Leu 260	Lys	Lys	Gln	Asp	Lys 265	Thr	Gly	Ser	Met	Asn 270
Val	Ile	His	Met	Leu 275	Glu	Ser	Phe	Thr	Phe 280	Arg	Asn	His	Val	Cys 285
				290				_	295	_			Ile	300
-		-		305	-				310			J	Lys	315
Ala	Gln	Ser	Ile	Leu 320	Gln	Ser	Leu	Asp	Ala 325	Leu	His	Lys	Asn	330
			-	335		_			340				Lys	345
				350					355				Ser	360
		_		365		_		_	370			_	Phe	375
				380					385				Pro	390
				395					400				Thr	405
				410					415				Ala	420
				425					430				Glu	435
				440					445				Pro	450
Tyr	Cys	Ser	Val	Thr	Thr	Gln	Ala	Asp	Gly	Arg	Val	Val	Leu	Val

				455					460					465
Gly	Gly	Arg	Ser	Arg	Arg	Gly	Lys	Lys	Arg	Gly	${\tt Pro}$	Pro	Gly	Ser
				470					475					480
Lys	Asp	Trp	Gly	Thr	Ala	Leu	Lys	Gly	Cys	Asp	Asp	Tyr	Leu	Phe
				485					490					495
Ile	Glu	Phe	Leu	Lys	Arg	Cys	Leu	His	Trp	Asp	Pro	Ser	Ala	Arg
				500					505					510
Leu	Thr	Pro	Ala	Gln	Ala	Leu	Arg	His	Pro	Trp	Ile	Ser	Lys	Ser
				515					520					525
Val	Pro	Arg	Pro		Thr	Thr	Ile	Asp		Val	Ser	Gly	Lys	Arg
				530					535					540
Val	Val	Asn	Pro	Ala	Ser	Ala	Phe	Gln	Gly	Leu	Gly	Ser	Lys	Leu
				545					550					555
Pro	Pro	Val	Val	-	Ile	Ala	Asn	Lys		Lys	Ala	Asn	Leu	Met
				560					565					570
Ser	Glu	Thr	Asn	-	Ser	Ile	Pro	Leu	Cys	Ser	Val	Leu	Pro	Lys
				575					580					585
Leu	Ile	Ser												
<210> 25														
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<211> 389

<212> PRT

<213> Homo sapiens

<220>

<221> misc feature

<223> Incyte Clone Number: 346275

<400> 25

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Ser Asp Phe Gly Leu Ser Lys Met Glu Gly Lys Gly Asp Val Met 200 205 Ser Thr Ala Cys Gly Thr Pro Gly Tyr Val Ala Pro Glu Val Leu 220 215 Ala Gln Lys Pro Tyr Ser Lys Ala Val Asp Cys Trp Ser Ile Gly 230 235 Val Ile Ala Tyr Ile Leu Leu Cys Gly Tyr Pro Pro Phe Tyr Asp 250 Glu Asn Asp Ser Lys Leu Phe Glu Gln Ile Leu Lys Ala Glu Tyr 265 Glu Phe Asp Ser Pro Tyr Trp Asp Asp Ile Ser Asp Ser Ala Lys 280 Asp Phe Ile Arg Asn Leu Met Glu Lys Asp Pro Asn Lys Arg Tyr 295 Thr Cys Glu Gln Ala Ala Arg His Pro Trp Ile Ala Gly Asp Thr 310 Ala Leu Asn Lys Asn Ile His Glu Ser Val Ser Ala Gln Ile Arg 320 325 Lys Asn Phe Ala Lys Ser Lys Trp Arg Gln Ala Phe Asn Ala Thr 335 340 Ala Val Val Arg His Met Arg Lys Leu His Leu Gly Ser Ser Leu 355 Asp Ser Ser Asn Ala Ser Val Ser Ser Ser Leu Ser Leu Ala Ser 365 370 Gln Lys Asp Cys Ala Tyr Val Ala Lys Pro Glu Ser Leu Ser 380 385

<210> 26

<211> 343

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone Number: 283746

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Cys Ser Phe Leu Asp Asp Leu Leu Glu Leu Arg Asp Glu Glu Leu
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Ser Lys Glu Ser Gln Glu Thr Asn Trp Phe Ser Ala Pro Ser Ala
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Leu Arg Val Tyr Gly Gln Tyr Leu Asn Leu Asp Lys Asp His Asn
Gly Met Leu Ser Lys Glu Glu Leu Ser Arg Tyr Gly Thr Ala Thr
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Met Thr Asn Val Phe Leu Asp Arg Val Phe Gln Glu Cys Leu Thr
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Tyr Asp Gly Glu Met Asp Tyr Lys Thr Tyr Leu Asp Phe Val Leu
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                                     220
Ala Leu Glu Asn Arg Lys Glu Pro Ala Ala Leu Gln Tyr Ile Phe
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Lys Leu Leu Asp Ile Glu Asn Lys Gly Tyr Leu Asn Val Phe Ser
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Leu Asn Tyr Phe Phe Arg Ala Ile Gln Glu Leu Met Lys Ile His
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Gly Gln Asp Pro Val Ser Phe Gln Asp Val Lys Asp Glu Ile Phe
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Asp Met Val Lys Pro Lys Asp Pro Leu Lys Ile Ser Leu Gln Asp
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<212> PRT

<213> Homo sapiens

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<221> misc_feature

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<210> 29

<211> 118

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<213> Homo sapiens

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<211> 356

<212> PRT

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<223> Incyte Clone Number: 2054049

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 15
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 Leu
 Gln
 Ala
 Ala
 Ala
 Gln
 Ser
 His
 Lys
 Ile
 Phe

 Leu
 Ala
 Arg
 Pro
 Ser
 Val
 Asn
 Ala
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 Lys
 Ala

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 Arg Thr Ala Gln Leu Thr Ser Leu Ala Met Leu Met Leu Asp Gly
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 Tyr Tyr Arg Thr Ile Arg Gly Phe Glu Val Leu Val Glu Lys Glu
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<213> Homo sapiens

<221> misc_feature

<223> Incyte Clone Number: 2843910

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Phe	Gln	Arg	Glu	Gln 65	Glu	Asn	Lys	Ser	Arg 70	Pro	His	Ser	Arg	Gly 75
Glu	Tyr	Asn	Val	Tyr 80	Ser	Thr	Phe	Gln	Ser 85	His	Glu	Pro	Glu	Phe 90
				Ser 95					100					105
				Gln 110					115					120
				Ile 125					130					135
				Tyr 140					145					150
				Ile 155					160					165
	_			Val 170					175					180
				His 185					190					195
				Ser 200					205					210
				Asp 215					220					225
				Glu 230					235					240
				Cys 245					250					255
				Cys 260					265					270
				Phe 275					280					285
				Ile 290					295					300
				Tyr 305					310					315
				Asn 320					325					330
				335					340					Asn 345
				350					355					Asp 360
				365					370)				Phe 375
				380					385	,				Glu 390
				395					400)				Thr 405
				410)				415	5				420
				425	5				430)				435
Val	. Ile	a Ala	ı Val	L Ala	ı Ala	Thr	Asr	ı Asr	ı Leı	туз	. TT6	e Phe	الم ال	Asp

445

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450

Lys Ile Asn

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<213> Homo sapiens

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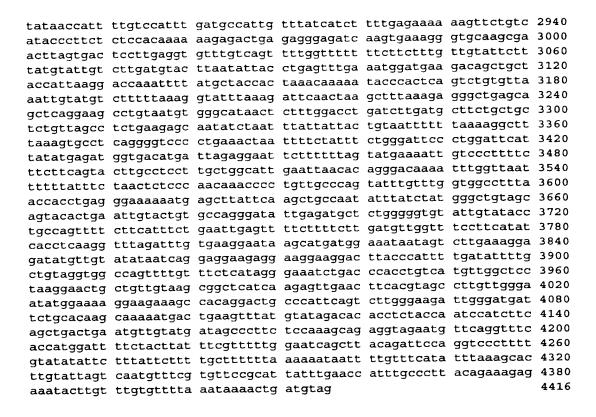
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Leu Ala Arg Ala Lys Ser Val Pro Thr Lys Thr Tyr Ser Asn Olu 290 295 Val Val Thr Leu Trp Tyr Arg Pro Pro Asp Val Leu Leu Gly Ser 305 310 Thr Glu Tyr Sor Thr Pro Ile Asp Met Trp Gly Val Gly Cys Ile 320 325 His Tyr Glu Met Ala Thr Gly Arg Pro Leu Phe Pro Gly Ser Thr 335 340 Val Lys Glu Glu Leu His Leu Ila Phe Arg Leu Leu Gly Thr Pro 350 Thr Glu Glu Thr Trp Pro Gly Val Thr Ala Phe Ser Glu Phe Arq 370 375 The Tyr Ber Phe Pro Cys Tyr Leu Pro Gin Pro Leu Ile Aen His 380 385 Ala Pro Arg Leu Asp Thr Asp Gly Ilc His Lou Lou Bor Bor Lou 395 400 Lou Lou Tyr Glu Ser Lys Sor Arg Met Ser Ala Glu Ala Ala Leu 410 415 Ser His Ser Tyr Phe Arg Ser Leu Gly Glu Arg Val His Gln Leu 425 43 D Glu Asp Thr Ala Ser lie Phe Ser Leu Lyz Glu Lie Gln Leu Gln 440 445 Lys Asp Pro Gly Tyr Arg Gly Leu Ala Pha Gln Gln Fro Gly Arg 455 45D Oly Lys Asn Arg Arg Gln Ser Ile Phe 470

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Aan	T i a	Leu	Leu		Acn	Glu	Phe	Ris		Lva	Ile	Ala	Авр	Pho
112.11				155					160	-1-			•	165
Glv	Leu	β∉⊼	Lys	Tro	Arg	Met	Met	Eer	Lau	Sar	Gln	ser	Arg	Ser
				170					175					180
Ser	Ĺув	Ber	Ala	Pro	Glu	Gly	Gly	Thr	Ile	31e	Tyr	Net	Pro	Pr≎
	-			185					190					195
Glu	Aen	Tyr	Glu	Pro	Gly	Gln	Lys	Эст	Arg	Ala	8er	Ile	Lyrs	
				200					205					210
Asp	Γla	Tyr	8er		Ala	val	lle	Thr		Glu	Lev	Leu	Ser	
				215	_			_	220		~1	_,		225
Lys	Gln	Pro	Ph¢		पुरार्भ	Val	Thr	ABD		Leu	Gin	IIB	Met	
				230		*	T	rr. 1	235	3	лı	<i>7</i> 15.	0-4	240
Ber	AST	Ser	$_{ m Glv}$		RIE	Arg	Pro	VAI	250	WB11	GIU	AT #	B-C-Y	255
	m	3 44	Ila	245	U i n	b	B.3 =	Tuesday		тъ	Rot	T.eni	Tla	
X.E.D	тут	нир	TTG	260	DT B	wrā	THA	ur A	265	116	361	Dea	110	270
Anv	Glw	Ten	Ala		Aen	Pro	Aero	Glu		Pro	9er	Phe	Leu	
n-ar	CLY	111	TILLE	275	11611		F		280					235
CVS	Leu	Iie	Gl u		Glu	Pro	Val	Leu	Arg	Thr	Fhe	Glu	Glu	Ile
-,-		•		290					235					300
Thr	Pha	Leu	Glu	Ala	Val	Ile	Gln	Leu	Lys	Lys	Tite	Lyz	Leu	Gln
				305					310					315
Ser	Val	9er	Ser	Ala	ile	His	Leu	Сув	geA	Lys	Lys	Lys	Met	
				320					325		_			330
Геп	Ber	Leu	Ago		Pro	Val	Asn	Ria		Pro	GIn	Olu	Glu	
	_			335	_			_	340		~	n	~ 1	345
Сув	Gly	Ser	Ser		Lец	His	GII	Apn		йТХ	Ret	PEO	G LU	360
	7		Lou	350	• ? -	D-c	/ 10 m	8 oc	355	n em	D'na	T.GO	Ser	
REL	WEG	Ser	MOU	365	HEA	LTO	3411	мзр	370	nop	1.10	печ	-	375
Lozie	Z la	G) n	Авр		TVT	₽he	Met	LVE		Bie	Hie	Cys	Pro	
-,-			···	390				•	395			-		390
Aen	Rie	Sex	Trp	Aco	₽e#	Thr	De	Ber	Gly	Ser	Glo	Arg	Ala	Ala
			-	395					400					405
Phe	Cya	Авр	Hie	LyE	Thr	Thr	Pro	Cyc	Ser	Ser	Ala	Ile	Ile	Yen
				410					415					420
Pro	Lev	9er	Thr	Ala	. Gly	Asn	Ber	Glu			Gln	Pro	Gly	
				425					430					435
Ala	Gla	GlE	ттр			. Ser	Lyc	Yrq			Ilo	Val	ASA	Gln
				440		_	417	a	445		61-	T 011		450
Met	Thr	Giv	r MTS			nea .	: 151111	. ser	450		ATO	. Den	LHOU	8er
T			. т].	455 Wet		മീവ	Lar	TI COMP			Ual	Деч	The	Lys
ALT	- wal	, Tuber	1 TT-	470			, Au		475					400
Pro	ም ከ ፣	- 2 mg	r The			. Wal	Aro	r Ġla			. Aat	Thi	The	Азр
			,	489			a	,	490					495
Ile	Gl	. Gly	/ Gl:			Ala	Lys	Val			Glr	Lye	Lev	Lys
				500)				505	i				510
Ast	. Ааг	ı Lye	e Glo	ı Met	: Gly	, Leu	ı Gle	Pro	тух	Pro) Glu	ı Ile	s Lev	. Val
_				515	5				520	}				525
Val	. 9e	e Ar	3 9ca			: Leu	а Аяс	ı Lev			ı Ası	ı Lıyı	# Bex	Met
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Ala Lys Thr Asp Tie Asn Cys Gly Thr Asp Leu Net Pho Tyx Ile
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Glu Met Asp Pro Sto Ala Lou Bro Pro Lys Pro Pro Lys Pro Thr
Thr Val Ala Aen Aan Gly Met Asn Aen Aon Mot Bar Leu Gln Asp
                  50
                                      55
Ala Glu Trp Trr Trp Gly Asp Ile Ser Arg Glu Glu Val Aen Glu
                                      70
Lys Leu Arg Asp Thr Ala Asp Gly Thr Pha Lou Val Arg Asp Ala
                  60
                                      65
Ser Thr Lys Met His Gly Asp Tyr Thr Leu Thr Leu Arg Lye Gly
                  95
                                     100
Gly Asn Asn Lye Leu Ile Lye Ile Phe His Arq Asp Gly Lya Tyr
                110
                                     115
Gly Phe Ser App Pro Leu Thr Phe Ser Ser Val Val Glu Leu Ila
                125
                                     130
Asn His Tyr Arg Asn Glu Ser Leu Ala Gln Tyr Asn Fro Lys Leu
                140
                                     1.45
Amp Val Lys Leu Lau Tyr Pro Val Ser Lys Tyr Gin Gin Amp Gin
                                     150
Val Val Lys Glu Asp Asn Ile Glu Ala Val Giy Lys Lys Leu Ris
                 170
                                     175
Glu Tyr Asn Thr Gln Phe Gln Glu Lys Ser Arg Glu Tyr Asp Arg
                                     190
                                                          195
Leu Tyr Glu Glu Tyr Thr Arg Thr Ser Gln Glu Ile Gln Met Lye
Arg Thr Ala Ile Glu Ala Phe Asn Glu Thr Ile Lys Ile Phe Glu
                                     220
Glu Gln Cys Gln Thr Gln Glu Arg Tyr Ser Lys Glu Tyr Ile Glu
                 230
                                     235
Lys Phe Lys Arg Glu Gly Agn Glu Lys Glu Ile Gln Arg Ile Met
                 245
                                     250
His Asn Tyr Asp Lys Leu Lys Ser Arg Ile Ser Glu Ile Ile Asp
                 26û
                                     265
Ser Arg Arg Arg Leu Glu Glu Asp Leu Lys Lys Gln Ala Ala Glu
                 275
                                     280
Tyr Arg Glu Ile Asp Lys Arg Met Asn Ser Ile Lys Pro Asp Leu
                 290
                                     295
Ile Gln Lou Arg Lys Thr Arg Asp Gln Tyr Lou Met Trp Lou Thr
                 305
                                     310
Gln Lys Gly Val Arg Gln Lys Lys Leu Aan Glo Trp Leu Gly Asn
                 320
                                     325
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340

Glu Asn Thr Glu Asp Gln Tyr Ber Leu Val Glu Asp Asp Glu Asp

335

Leu Pro His His Asp Glu Lys Thr Trp Asn Val Gly Ser Ser Asn 259 Arg Asn Lys Ala Glu Asn Leo Leo Arg Oly Lys Arg Asp Gly Thr 370 365 Pha Leu Val Arg Glu Ser Sor Lys Gln Gly Cys Tyr Ala Cys Ser 385 360 Val Val Val App Cly Glu Val Lya Gis Cys Val Ile Asn Lys Thr 395 400 Ala Thr Gly Tyr Gly Phe Ala Glu Pro Tyr Asn Leo Tyr Ser Ser 415 410 Leu Lys Glu Lou Val Lou His Tyr Gln His Thr Ser Leo Val Gln 430 425 His Asn Asp Ser Leu Asn Val Thr Lou Ala Tyr Pro Val Tyr Ala Glo Glo Arg Arg

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<213> Home capiens

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215
                                     220
                                                         225
Lys Met Wro Asp Val Glu Leu Phe Val Asn Leu Gly Asp Trp Pro
                230
                                     235
Leu Glu Lys Lys Ser Asn Ser Azn Ile Hig Pro Ile Phe Ser
                245
                                     250
Trp Cys Gly Ser Thr Asp Ser Lys Asp Ile Val Met Pro Thr Tyr
                260
                                     265
                                                         270
Asp Leo Thr Asp Ser Vel Leo Glu Thr Met Gly Arg Val Ser Leu
                275
                                                         285
Asp Met Met Ser Val Glm Ala Asn Thr Gly Pro Pro Trp Glu Ser
                290
Lys Agn Ser Thr Ala Val Trp Arg Gly Arg Asp Ser Arg Lys Glu
                                     310
                                                         315
Arg Leu Glu Leu Val Lys Leu Ser Arg Lys His Pro Glu Leu Ile
                320
                                     325
Asp Ala Ala Phe Thr Asn Phe Phe Phe Lyz Hiz App Glu Asn
                335
                                     340
Leu Tyr Gly Pro Ile Val Lys Ris Ile Ser Phe Phe Asp Phe Phe
                350
                                     355
Lys His Lys Tyr Gln He Asn He Asp Oly Thr Val Ala Ala Tyr
                365
                                     370
                                                         375
Arg bed Pro Tyr Leu Leu Val Gly Asp Ser Val Val Leu Lys Gln
                36D
                                     385
                                                         390
Amp Ser Ile Tyr Tyr Glu His Phe Tyr Amn Glu Leu Gln Pro Trp
                395
                                     400
                                                         405
Lys His Tyr Ile Pro Val Lys Ser Asn Lau Sar Asp Leu Leu Glu
                410
                                     415
                                                         420
Lys Leu Lys Trp Ala Lys Asp Riz Azp Glu Glu Ala Lys Lys Ile
                425
                                     430
                                                         435
Ala Lys Ala Gly Gln Glu Phe Ala Arg Asn Asn Leu Met Gly Asp
                440
                                     445
                                                         450
Asp Ile Phe Cys Tyr Tyr Phe Lys Leu Phe Gln Glu Tyr Ala Aen
                455
                                     460
Leu Gla Val Ser Glu Pro Gla Ils Arg Glu Gly Met Lys Arg Val
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Glu Pro Gln Thr Glu Asp Asp Leu Phe Pro Cys Thr Cys His Arg
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 Pro Pro Pro Pho Trp Asp Glu Asp Gln Ris Arg Leu Tyr Gln Gln Ile
 20
 25
 30

 Lys Ala Gly Ala Tyr Asp She Pro Ser Pro Glu Typ Asp Thr Val
 35
 40
 45

PCT/US99/17132 WO 00/06728

Thr Pro Glu Ala Lys Asp Leu Ila Asn Lys Met Leu Thr Ila Asn E0 Pro Ala Lys Arg lls Thr Ala Ser Glo Ala Leu Lys His Pro Trp 70 65 Ile Cys Gln Arg Ser Thr Val Ala Ber Met Met His Arg Gln Glu 85 80 The Val App Cys Lou Lys Lys Phe Asn Ala Arg Arg Lys Leu Lys 100 95 Gly Ala Ile Leu Thr Thr Met Leu Ala Thr Arg Asn Pho Ser Ala 115 Ala Lys Ser Leu Leu Lys Lys Pro Asp Sly Val Lys Glu Ser Thr 130 125 Glu Ser Ser Asn Thr Thr The Glu Asp Glu Asp Val Lys Ala Arg 145 140 Lys Gln Glu Ile Ile Lys Val Thr Glu Gln Leu Ile Glu Ala Ile 160 Asn Asn Gly Asp Phe Glu Ala Tyr Thr bys Ile Cys Asp Pro Gly 175 170 Lou Thr Ala Phe Glo Pro Glu Ala Leu Gly Aen Leu Val Glu Gly 190 135 Met Asp Phe His Arg Phe Tyr Phe Glu Asn Ala Leu Ser Lys Ser 200 Asn Lys Pro Ile His Thr Ile Ila Lau Asn Pro His Val His Lau 220 215 Val Gly Asp Asp Ala Ala Cys Ile Ala Tyr Ile Arg Leu Thr Gin 230 235 Tyr Met Asp Gly Ser Gly Net Pro Lys Thr Met Gln Ser Glu Glu 250 245 Thr Arg Val Trp His Arg Arg Asp Gly Lys Trp Gln Asn Val His 265 360 Phe His Arg Ser Gly Ser Pro Thr Val Pro Ile Asn 275

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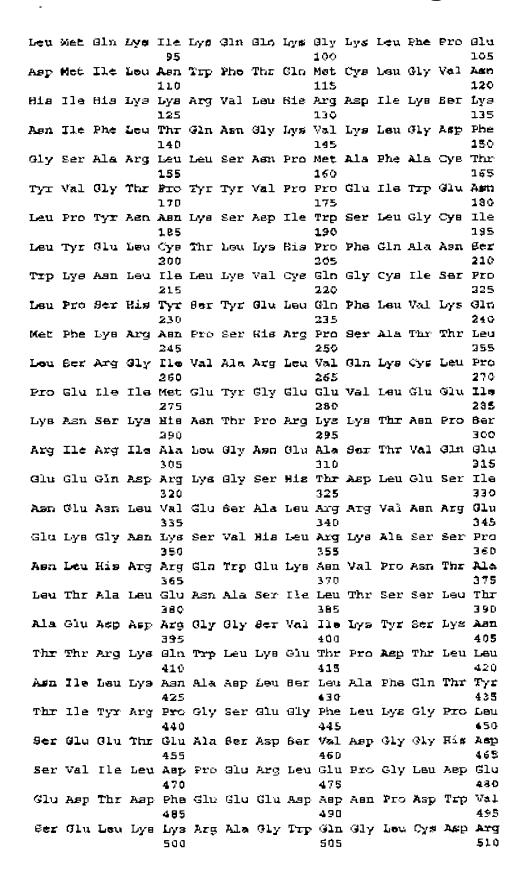
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The Pro Cys Pro Ser Ile Leu Glu Leu Glu Glu Leu Leu Arg Ala
Gly Lye Ser Ser Cye Ser Arg Val Asp Glu Val Trp Pro Asn Lou
The Ile Cly Asp Ala Met Asp Ser Leu Glo Lye Glo Asp Leu Arg
Arg Fro Lys Ile Ris Gly Ala Val Gla Ala Sor Pro Tyr Gla Pro
Pro Thr Leu Ala Ber Leu Gln Arg Leu Leu Trp Val Arg Gln Ala
Ala Thr Leu Asn His Ile Asp Glu Val Trp Pro Ser Lou Phe Leu
                 95
                                    100
Oly Asp Ala Tyr Ala Ala Arg Asp Lys Ser Lys Leu Ile Gln Leu
                                    115
                110
Gly Ile Thr His Val Val Agn Ala Ala Ala Gly Lys Pho Gln Val
                125
                                    130
Asp Thr Gly Ala Lys Phe Tyr Arg Gly Met Ber Leu Glu Tyr Tyr
                140
                                    145
Cly fle Glu Ala Asp Asp Asn Pro Phe Phe Asp Leu Ber Val Tyr
                155
                                     160
Phe Leu Pro Val Ale Arg Tyr Ile Arg Ala Ala Leu Bor Val Pro
                170
                                    175
Gin Gly Arg Val Leu Val His Cys Ala Ket Gly Val Ser Arg Ser
                185
                                     190
Ala Thr Leu Val Leu Ala Phe Leu Met Ilo Tyr Glu Asn Mot Thr
                200
                                     205
Low Val Glu Ala Ila Gln Thr Val Gln Ala His Arg Aen Ile Cys
                215
                                     220
Pro Ash Ser Cly Pho Leu Arg Cln Leu Cln Val Leu Asp Ash Arg
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Leu Gly Arg Glu Thr Gly Arg Phe
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	Pro		Gln	Gly 5	Glu	Aep	Сув	Тут	Phe 10	Phe	₽he	Tyr	9 er	Thr 15
Суп	The	Lys	Gly	Asp 20	Ser	Cye	Pro	Phe	Arg 25	Híg	Сув	Glu	Ala	Ala 30
	e Gly			35					40			_		4,5
	. Arg			50					55			_	-	50
	, Ber			65					70					75
	Lye			90					95			•	_	90
	Qly			95					100					105
	Glu			110					115					120
	Gln -			125					130					135
	ger 			140					145					150
	His			155					160					165
	Aep			170					175			·		180
	Leu			165					190	_		_		195
	Val			200					205				-	210
	. Fhe			215					220	_		_	-	225
	Glu Lou	_		230			_		235			-		240
	Leu Val			245					25 0	_			_	255
	. vai			260					265					270
	Azg			275					280			_		285
	Ser			290					295					300
	: Aan			305					310					315
	Lys			320					325				•	330
	The			335					340					345
	Glu			350					355				-	360
	สโจ			365					370					375
	Thr			360					365					390
	e Ser			395					400					405
				•			•	-		-				

				410					415					42D
Glu	Ara	Gln	Lva		Lve	Lve	Ago	Thr		Ove	Ile	Lvs	Leu	
			-4-	425	_, _	-,-	•		430			- • -		495
Lie	Asp	9¢r	Glu	Ile	Lys	Lys	The	Val	Val	Leu	Pro	PTO	11=	Val
				440	-	••			445					650
Als	ser	Arg	Gly	Gln	Ser	Glu	Glu	Pro	Ala	Oly	Lys	Thr	Lys	9er
				455					460					465
Met	Gl n	Gl u	Vel	Hig	Il¢	$\Gamma^{\lambda k}$	The	Lou		Glu	Ila	Lya	Fen	
				470	_	_		_	175	_	_		_	480
ГАВ	Ala	Lau	Arg		Gln	Gln	Ber	Ser		ser	ser	Thr	Ser	
T)	0		Tr. Law	485	B 1 ±	IFTL -	D	<i>.</i>	490	T	Tracer	Timosa	T.an	495
FXO	eer	ήΥΩ	HIB	500	ALG	7111	RIO	GIA	205 204	wrg	wr. A	пып	Lau	510
Tle	Thr	T.V.A	Агп		Glv	Met	LVB	ផារ		IME	Aan	Leu	Gln	
110		272		515					520	,-				525
Oly	Asrı	Gl a	Val	•	Ser	Gla	Вег	Oor		Arg	Thr	Glu	Ala	Lye
•				530					535					540
Glu	Ala	Ber	Gly	Glu	Thr	Thr	Gly	Val	Авр	lle	Thr	Lys	Ile	
				545					550					555
Val	Lys	yrd	Cy #		1. Jr. 1.	Met	Arg	Glu	-	His	Net	gln	Lув	
-47	447		-e-a	560		ne- 1	·	mЪ _	565	T	7	~ 3) ar	570 Vol.
GII	GIU	Arg	GIU	Ly <i>a</i> 575	Ser	Val	Leu	THE	580	тъп	Arg	нтА	Asp	585
n l m	Oer-	Cycer	ā en		G1 m	Ua1	21.4	(31 m		b ተ	ra 1	T.=11	Thr	
AL 4	0 - 1	+3.4	W-11-11	590	4+11	• 4	P-+	714	595	210	447	D-0-0		600
Val	Pro	Glv	Ile		Arg	нів	Leu	Thr		Arg	Leu	Pro	Thr	
		•		505	_				610	_				615
Ser	0er	G1n	Lys	Val	Glu	Val	\mathbf{Glu}	Thr	Ber	Gly	ile	${\tt Gly}$	qeA	Set
				620					625					630
Lau	Leu	Aso	Val	_	Сув	Ala	Ala	Gln		Leu	Glu.	Lys	Arg	
_		_	_	635 -			1	.	54ŭ	a .			T	645
Lys	YIE	Lys	Pro	€20 TÀS	AST	AEN	VAL	TÀ	655	Rez	AST	AMT	Lys	€60 ART
32 - 3	Ae-	Ser	Pro		Tazm	Ala	Proc	LWB		TAVE	Ala	val	Glu	
7 (4)		PO#	-10	665	1101			,	670	_,_				575
Bia	Ala	Ala	Val		Ala	als	Val	Lye	Pro	£eu.	9er	Ber	Ser	9er
				690					605					690
Val	Leu	Gla	Glu	Pro	Pro	Ala	Lys	Ĺув	Ala	Ala	Val	Ala	Val	
				695				_	700					705
Pro	Γeπ	Val	Ser			Lye	Ser	Val		Vel	Ъţф	Glu	FIR	Glu
_		_		710					715		-3-	~	~	720
Asn	Pro	Arg	ABD			var	LBU	PLO.	730	Thr	GID	ser	361	8er 735
Aer.	Car	Car	- Dec	725 Pro		ប្ចារ	Ser	สาง		Spinger	Ser	Ser	Gln	Met
بإصد	CLI		110	740		• • • •		,	745		T-			750
Ser	Net	Lys	Thr		Arg	Ĺsu	Ber	Ber			Thr	Gly	Lye	Pro
				7 55					750					765
Pro	Leu	Ser	Val	Glu	Aep	Авр	Ph≞	gjų,	រូបិន	Lou	Ila	Try	Glu	lle
				770					775				_	780
Set	Gly	Gly	Lya			Ala	Glu	Ile			A Ep	Pro	Gly	Гув
_		_	_	7 8 5					790			-1		795
AKP	ĠΤΰ	A##	Aab			, ь∉ч	. Glu	_ ECU			Mat	TT-8	- Азр	8 6 #
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His Ala His Cly Gin Ile Glo Val Arg Gln Leu Phe Glu Asp Asn
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Ser Asn Lys Arg Thr Val Leu Thr Thr Gln Pro Asn Gly Lou Thr
                 50
                                      55
Thr Val Gly Lys Thr Gly Lou Pro Val Val Pro Glu Arg Gln Leu
                 65
                                      70
Asp Ser lie Wis Arg Arg Gln Gly Ser Ser Thr Ber Leu Lys Ser
                                      85
                 ŪŪ
Met Glu Gly Met Gly Lys Val Lys Ala Thr Pro Met Thr Pro Glu
                                     100
Gln Ala Met Lye Gln Tyr Met Gln Lye Leu Thr Ala Fhe Glu Hie
                110
                                     115
His Glu Ile Phe Ser Tyr Pro Glu Ile Tyr Phe Leu Gly Leu Asn
                                     130
                1.25
Ala Lys Lys Arg Gln Gly Met Thr Gly Gly Pro Aso Aso Gly Gly
                                     145
Tyr Asp Asp Asp Gln Gly Ser Tyr Val Gln Val Fro His Asp His
Val Ala Tyr Arg Tyr Glu Val Lou hys Val Ilc Gly Lys Gly Her
                 170
                                     175
Phe Gly Gln Val Val Lys Ala Tyr Asp His Lys Val His Gln His
                                     190
Val Ala Leu Lys Met Val Arg Asn Glu Lys Arg Pho His Arg Glm
Ala Ala Glu Glu Ile Arg Ile Leu Glu His Leu Arg Lye Gln Asp
Lys Asp Asn Thr Met Asn Val Ile His Met Leu Glu Asn Phe Thr
                 230
                                     235
Phe Arg Asn His Ile Cys Met Thr Phe Glu Leu Leu Ser Met Asn
                 245
                                     250
Leu Tyr Glu Leu Ile Lye Lys Asn Lye Phe Gln Gly Phe Sex Leu
Pro Leu Val Arg Lys Phe Als His Ser Ile Leu Gln Cys Leu Asp
                 275
                                     290
Ala Leu His Lys Asn Arg Ile Ile His Cys Asp Leu Lys Pro Glu
                 290
                                     295
Asn Ile Leu Leu Lys Gin Gin Gly Arg Ser Gly Ile Lys Val Ile
                 305
                                     310
Amp Phe Gly Ser Ber Cys Tyr Glu Him Gln Arg Val Tyr Thr Tyr
                                     325
                 320
Ile Gin Ser Arg Phe Tyr Arg Ala Pro Glu Val Ile Leu Gly Ala
                                     340
                 335
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Arg Tyr Gly Met Pro Ile Asp Met Trp Eer Leu Gly Cys Ile Leu

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350
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Ala Glu Leu Leu Thr Gly Tyr Pro Leu Leu Pro Gly Glu Asp Glu
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                                     370
                                                          375
Gly Asp Gln Lou Ala Cys Met Ile Glu Leu Leu Gly Met Pro Ser
                 320
                                     385
Gln Lys Lou Leu Asp Ala Ser Lys Arg Ala Lys Asn Pho Val Ser
                 395
                                     400
Ser Lys Gly Tyr Pro Arg Tyr Cys Thr Val Thr Thr Leu Ser Asp
                 410
                                     415
Gly Sar Val Val Leu Asn Gly Gly Arg Ser Arg Arg Gly Lys Leu
                 425
                                     430
Arg Gly Pro Pro Glu Ser Arg Glu Trp Gly Asn Ala Leu Lys Gly
                 440
                                     445
Cys Asp Asp Pro Lew Phe Lew Asp Phe Lew Lys Gin Cys Lew Glu
                455
                                     46D
Trp Asp Pro Ala Val Arg Met Thr Pro Gly Gla Ala Leu Arg His
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                                     475
Pro Trp Let Arg Arg Arg Let Pic Lys Pro Pro Thr Gly Glu Lys
                495
                                     490
Thr Ser Val Lya Arg Ile Thr Glu Ger Thr Gly Ale Ile Thr Ser
                                     505
The Ser Lys Lau Pro Pro Pro Ser Ser Ser Ala Ser Lys Leu Arg
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Arg Thr Val Lau Pro Lys Leu Val Ser
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125
Lys Ala Mot Glu Ser Lys Lys Thr Tyr Glu Gln Lys Cys Arg Aep
                14Û
                                    145
Ala Amp Amp Ala Glu Gin Ala Phe Glu Arg Ile Ser Ala Amn Gly
                155
                                    160
His Gin Lys Gin Val Glu Lys Bor Cin Asn Lys Ala Arg Gin Cys
                170
                                    175
Lys Asp Ser Ala Thr Glu Ala Glu Arg Val Tyr Arg Gln Ser Ile
                185
                                    190
Ala Gln Leu Glu Lys Val Arg Ala Glu Trp Glu Gln Glu His Arg
                200
                                    205
Thr Thr Cya Glu Ala Phe Gln Leu Gln Glu Phe Amp Arg Leu Thr
                215
Ile Lou Arg Asn Ala Leu Trp Val His Ber Aen Gln Leu Ser Met
Gin Cys Val Lys Asp Glu Leu Tyr Glu Glo Val Arg Leu Thr
                                    250
Leu Glu Gly Cys Ser Ile Asp Ala Asp Ile Asp Ser Phe Ile Gln
                250
                                    365
Ala Lys Ser Thr Gly Thr Glu Pro Pro Ala Pro Val Pro Tyr Gln
                275
                                    280
                                                         265
Asn Tyr Tyr Asp Arg Glu Val Thr Pro Leu Thr Ser Ser Pro Gly
                290
                                    295
                                                         300
Ile Gln Pro Ser Cys Gly Met Ile Lys Arg Pho Ser Gly Leu Leu
                305
                                    310
His Gly Ser Pro Lys Thr Thr Ser Leu Ala Ala Ber Ala Ala Ser
                320
                                    325
Thr Glu Thr Leu Thr Pro Thr Pro Glu Arg Asn Glu Gly Val Tyr
                335
                                    340
Thr Ala Ile Ala Val Glo Glu Ile Glo Gly Asn Pro Ala Ser Pro
                350
                                    355
Ala Gin Glu Tyr Arg Ala Leu Tyr Asp Tyr Thr Ala Gin Asm Pro
                365
                                    370
Amp Glu Leu Amp Leu Ser Ala Gly Amp Ils Leu Glu Val Ils Leu
                300
                                    385
Glu Gly Glu Asp Gly Trp Trp Thr Val Glu Arg Asn Gly Gln Arg
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                                    400
Gly Phe Val Pro Gly Ser Tyr Leu Glu Lys Leu
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<211 > 425

<212> PRT

<213> Homo sapiene

<220>

<221> misc_feature

<223> Incyte Clone Number: 1997814

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Gln Gly Glu Leu Glu Lys Leu Asn Gln Ser Thr Asp Asp Ile Asn
20 25 30
Arg Arg Glu Thr Glu Leu Glu Asp Ale Arg Gln Lys Phe Arg Ser

WO 00/06728 PCT/US99/17132

```
Val Leu Val Glu Ala Thr Val Lys bou Asp Glu Leu Val Lys Lys
Hie Gly Lya Ala Val Glu Asp Ser Lys Pro Tyr Trp Glu Ala Arg
                 65
                                     70
Arg Val Ala Arg Glo Ala Glo Leu Glu Ala Glo Lys Ala Thr Glo
                 80
Amp Phe Gin Arg Ale Thr Glu Val Leu Arg Ala Ala Lys Glu Thr
                                    100
                 95
Ile Ser Leu Ala Glu Gln Arg Leu Leu Glo Asp Asp Lya Arg Gln
                                    115
Phe Amp Ser Ala Trp Gln Glu Met Leu Amn His Ala Thr Gln Arg
                                    130
Val Met Glu Ala Glu Gln Thr Lys Thr Arg Ser Glu Leu Val His
                                    145
Lys Glu Thr Ala Ala Arg Tyr Asn Ala Ala Met Gly Arg Met Arg
                                    160
Gln Leu Glu Lys Lys Leu Lys Arg Ala Ile Asn Lys Ser Lys Pro
                                    175
Tyr Phe Glu Leu Lys Ala Lys Tyr Tyr Val Gln Lau Glu Gln Lau
                195
Lys Lys Thr Val Asp Asp Leu Gln Ala Lys Leu Thr Leu Ala Lys
                                    205
                200
Gly Glu Tyr Lye Met Ala Leu Lys Asn Leu Glu Met Ile Ser Asp
                                    220
                215
Glu Ile His Glu Arg Arg Fer Ser Als Met Gly Pro Arg Gly
                23 0
                                    235
Cys Gly Val Gly Ala Glu Gly Sar Ser Thr Ser Val Glu Asp Leu
                245
                                    250
Pro Gly Ser Lys Pro Glu Pro Asp Ala Ile Ser Val Ala Ser Glu
                                     265
                250
Ala Phe Glu Asp Asp Ser Cys Ber Asn Phe Val Ser Glu Asp Asp
                275
                                     280
Ser Glu Thr Gln Ser Val Ser Ser Phe Ser Ser Gly Pro Thr Ber
                                     295
                290
Pro 6er Glu Met Pro Asp Glo Phe Pro Ala Val Val Arg Pro Gly
                                     310
                                                         315
                 305
Ser Leu Asp Leu Pro Ser Pro Val Ser Leu Ser Glu Phe Gly Met
                                     325
                 320
Ket Phe Pro Val Leu Gly Pro Arg Ser Glu Cys 8er Gly Ala 9er
                                     340
                 335
Ber Pro Glu Cye Glu Val Glu Arg Gly Asp Arg Ala Glu Gly Ala
                                     355
Glu Asn Lys Thr Ser Asp Lys Ala Asn Asn Asn Arg Gly Leu Ser
                                     370
                 365
 Ser Ser Ser Gly Ser Gly Ser Ser Lys Ser Gln Ser Ser Thr
                                     385
 Ser Pro Glu Gly Gln Ala Leu Glu Asn Arg Met Lya Gln Leu Ser
 Leu Glm Cys Ser Lys Gly Arg Asp Gly He He Ala Asp He Lys
                 410
 Met Val Gln Ile Gly
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325

340

Lys Asp Glu Thr Glu Tyr Glu Tyr Ser Gly Ser Glu Glu Glu Glu

Glu Glu Val Pro Glu Glu Glu Gly Glu Fro Ser Ser He Val Asn

Val Pro Gly Glu Ser Thr Leu Arg Arg Asp Fha Leu Arg Leu Gla

320

335

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rea	CTI	Ġίй	OTU	380	теп	wrâ	GIU	GIII	365	GIU	+ } +	77.4		390
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Arm	AYYI	Arg	Len		alu	Glrı	Gln	Arq		Glu	Arg	Glu	Ala	Arg
	 <u>-</u>			410					415		_			420
Arq	Gln	Gln	Glu	AYG	Glu	Gln	Arg	Arg	Arg	Glu	Gln	Ğlu	Glu	Lys
-				425					430					435
Arg	Arg	Leu	Glu.	Glu	Leu	\mathbf{Glu}	Arg	Arg	Arg	Lys	Glu	Glu	Glu	Glu
				440					445					450
Arg	Arg	Arg	Ala	Glu	Glu	Glu	$L\gamma \kappa$	Arg		Val	Glu	Ψī	Glu	
				455			_	_	450		_			465
\mathbf{Glu}	Tyr	Ile	Arg		Gln	Leu	Glu	Glu		g) H	YLÜ	HIM	Leu	
			_,	470	•	•		W7	475	r. 7 =	31-4	T	Ton	460
Val	Leu	GΤυ	GLE		rea	L≑u	GIN	OT.I		WIE	vier.	Pen	TAR	A95
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Lve	Ala	нів	TVT		Pro	Ala	Asp	Arg		Arq	Glu	Val	Pro	Val
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Arg	Thr	Thr	Ser	Arg	Ser	Pro	Val	Leu	8er	Arg	Arg	Asp	Bor	Pro
_				545					5 5 0					555
L∉ņ	Gln	Gly	Ser	Gly	Glu	Gln	Asn	Ser	Gln	Ala	gly	Gin	Arg	Aen
				560					565					570
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	_			575			.45	_	560					585
Leu	Val	Pro	Arg		Gly	gor	GIY	ser		ser	GIY	201	251	500
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Pro	Ber	Gln	Arq			Asn	Ala	Val	Lys	Lys	Pro	Glu	Авр	Lys
				635					640					645
Lys	alu	Val	Ph¢	Arg	Pro	Leu	Lya	Pro	Ala	Asp	Leu	Thr	Ala	Lau
				650					655					660
Ala	Lys	Glu	Leu	Arg	Ala	Val	Glu	Yab			Pro	- Exo	His	Lyp
				565					670					675
Val	Thr	Asp	Туг			: Ger	Ser	Glu			GLY	Thi	THE	Д ЭД 690
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				770					775					780
alv	île	Ber	${\tt Prc}$	Ber	6er	Gly	Thr	Thr	val	Thr	ser	Val	Val	Gly
				785					790					795
Phe	Ser	Сув	q es		Met	भम्प्यु	Pro	Glu	Alm	Ile	Arg	ឲារជ	Азр	FTO
				8 0 0					605					810
Thr	Frg	ГÀв	Gly		Val	Val	Asn	Val		Pro	Thr	Aen	Thr	_
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Pro	⊕ln	9er	ywb		Pro	Glu	Ile	yig		Tyr	Γλ≥	Lyp	ΉτĠ	
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ABI	ber	GLU	Ile		cya	WT9	ата	Lau	-	GIÀ	Val	ABIL	Leu	
110.5	a1	mt. a.	Glu	845	~ 33	7	u	T	850	7	1	n	cm*1	855
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ett v	Two	17-1	Tyr		1 max	71.0	Jan	n seer		S. record	Sho	രവം	en e	
GLY	nys	AOLI	171	875	Dec	7.40	пан	n. 9	880	wrā	CIL	3411	GILL	885
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				890					695	7-10			1	300€
Lys	Asp	Lve	Leu		Val	Tyr	TVT	Leu		Tro	Lau	Arg	Aen	
•	-	-		905		•	•		910					915
Ile	Lou	Hio	Asn	App	Pro	Glu	Val	Glu	Lye	Lys	Gln	Gly	Trp	
				920					925			•	•	930
Thr	Val	Gly	Аєр	Leu	Gl u	Gly	Сув	Val	Нiв	туг	Lys	ſæV	Val	Lys
				935					94 D					945
$\mathbf{T}_{j'}\mathbf{r}$	a_{1a}	yrg	Il∉	Lye	Phe	rea	Val	Ile	Ala	L≞u	Lye	9er	Ser	Val
				950					955					960
31u	Val	Туг	Ala	_	Ala	Pro	Lys	Pro	_	Нiв	Ľув	Fhe	Net	Ala
_,	_	_		965		_			970	_	_	_ •		975
Ph€	Lye	ser	Phe	_	Glu	Leu	Val	1118	_	Ser	Cye	ALS	ary	
173 as	B.7 -	17-1	1	980	1	0.44	41. .	0	985	m	.	T 3 =		390
HIB	MIG	AGT	yab	995	чер	##E	ĢΨλ		LODO	Tyr	Азр	176		
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110				1010	-	0.51	110	_	1015	1110	71.2.4			1020
. Leu	Pro	Agn			Glv	Met	Glu			Val	Cva	Tvr		
	•	-		1025	•				1030			•		LOSS
Glu	Gly	Val	Tyr	Val	Asn	Thr	Tyr	Gly	Arg	Xle	Thr	Lys	Aep	Val
				1040			_	_	LD45			-	_	L050
Val	$L\!\!=\!\!u$	Gl#	Trp	Gly	Glu	Met	Pro	Thr	9er	Val	Ala	$\mathbf{T}_{\mathbf{J}'}\mathbf{r}$	I1¢	Arg
				1055					1060					L055
1e B	Aan	Gln	Thr	Ket	Gly	Trp	Ğlγ	Glu	Lув	Ala	Ile	Glu	Ile	ЖŢ
				1070					1075					L080
2 er	Val	Glu	Thr		Him	Leu	Aur	_		Pho	Not	Rig	_	
		_		1085			_		1090					1095
ЪТЯ	Gln	Arg	Leп		Phe	Leu	Сув		_	Azn	ysb	Lye		
Tola -		α.		1100	.				1105	447				1110
₽D Ç	ALA	ROL	Val		위수로	GTA	GIY			OTU	Val	LAS		
The	T .enr	⊘ 1+•		1115	60-	T	T 011		1120				•	11.25
1111	ıreıı	OT A.	Frd	TOF 1130	264	THOU	Ten		4rp 1 1 35					
			•	4434				•	***3					

<211> 223 <212> PRT

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<213> Homo sapiens

<220> <221> misc_feature <223> Incyte Clone Number: 209854

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<210> 16 <211> 503 <212> PRT <213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte Clone Number: 1384286

				50					55					<i>-</i>
Glu	Ala	Arg	Ile	Cys	Arg	Leu	Leu	Lyz	Hie	Ser	Asu	ĭ1=	Val	_
T +=== 13	Hia	Aep	ge.	65 41	9-+	G14:	(31 ₁)	Ø1 v	70 Bba	ui o	173.co	T 011	YF- 7	75 Pos
		-m-p		80			47.44	Gary	85	ULB	73.7	TASIT	vaa	90
Авр	Leu	val	Thr		Gly	Glu	Leu	Phe		Asp	Ile	Val	Ala	
_				95	_				100	_		•		105
Glu	$T\chi \pi$	Tyr	9er	Gl u	Ala	Asp	Ala	ßer	Hia	Сув	${\tt Ile}$	Gln	Gln	11e
			_	110				_	115	_				120
Leu	Glu	Ala	Val		нів	∴\a	Hie	Gln		Cly	VAl	Val	Hie	_
Acm	I 🖦 11	Lyn	Pro	125 (31):	Len	T 📤 Ya	Len	Len	130	Car	Y. rest	e e	Yarn	135 /31./
			• • • •	140			744	204	145	DOL	пую	Cyp	DJ 0	150
Ala	Ala	val	Lув	Leu	Ala	Авр	Phe	Gly		Ala	Ile	Glu	Val	
				155					160					165
Gly	Аэр	Gla	Gln		Tro	Phe	Gly	Pho		Gly	Thr	Pro	Gly	-
7 811	C. N	Fig. 2	~1	170	T 0.11	3	T		175	m	ed	.	T	180
п¢п	3-21	Pro	GIU	185	nen	мg	m), n	ЭТП	190	Tyr	ATA	PAB	t±0	195
Аэр	Ils	Trp	Ala		Gly	Val	Ile	Leu		Ile	Leu	Leu	Val	
-		_		200	•				205					210
Tyr	$Px \circ$	Pro	Ph≑	\mathbf{Trp}	Asp	Glu	Asp	3ltı	Bá¢	Lys	Lou	Tyr	G ln	Gin
	_	_ =	4.1	215					220					225
Ila	Lys	Ala	GLY	A1a 230	Tyr	ABP	Phe	Pro		Pro	Glu	Tip	qaA	
val	Thr	Pro	Glu		Lvs	Asn	Leu	Ile	235 Agn	aln	Met	Len	ጥክ የ	240 Tle
				245					250					255
Agn	$\mathbf{Pr} \diamond$	Ala	Lys	Arg	Il¢	Thr	Ala	His	Glu	Ala	Leu	Lys	His	Fixo
			_	260					265					270
Trp	Val	Cye	Gln		Ser.	Thr	Val	Ale		Met	Met	Hig	AYG	
Glu	Thr	Val	(ZI 11	375 Cve	Lenn	Lord	Ive	Sha	290	<u>ከ</u> ገ =	Arn	Den	Yaza	285 Lenn
				290		-,-	••, •	-110	295	71111	3	- -	11 0	300
Lys	Gly	Ala	Ile	Leu	Thr	Thr	Ket	Leu	Ala	Thr	Arg	Aen	Phe	Ser
	_			305					310					315
Ala	Ala	TÄR	₽♠∺		Г÷л	Aen	Lyg	lye		Asp	Oly	Val	Lors	
Hi a	The	Asn	Ear	320 Thr	Lize	Bon	Ear	215	325	ם דב	min se	Sev	Dva	330
1110		11011	-	335	272		001	7.10	340	шп	1 111	364	FIG	345
gly	Thr	Leu	Pro	Pro	Ala	Ala	Zeu	Glu		9ex	Asp	9ex	Ala	
				350					355					360
Thu	Thr	Ile	Glu		Glu	УвЬ	Ale	Lye		yzā	ГÀв	Gln	Glu	
T7.0	1	Th ~	frib	365	<i>3</i> 3	۲	77.	~ 17	370	17- 1			45	375
TTA	туу	Thr	TIIL	380	Gill	Ten	TTA	GTU	385	AST	HBII	ABI	GIÅ	390 390
Phe	31 u	ela	Tyr		Lye	Ile	Cys	Age		Glv	Leu	Thr	ser	
			_	395	•		-	•	400					405
Glu	Pro	Glu	Ala		$\operatorname{\mathfrak{a}\!\hspace{1pt} J} \lambda$	ಗಾನ	Leu	Val		Gly	Net	Азр	Phe	
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Arg	₽27 G	Туг	hVē		Aen	reu	гел	Als	_	ABN	Ser	Lye	Pro	
Hía	Thr	Thr	1la	425 Leu	Aso	Pro	Hi =	y,≘1	430 H1R	\ Tal	ትገ=	ជ្ឈា _ម	(1 3.55	435 Aaro
				440					445	+41		1	- 40 M	450
Ala	Ala	Сув	Ile	Ala	Tyr	Ile	Arg	Leu		Gln	Tyr	Ile	Asp	
		_		455					460					465
üln	gry	Arg	PTC	Arg	The	Sar	37 u	Ber	Glu	Glu	Thr	yxâ	Val	Trp

470 475 480

His Arg Arg Asp Gly Lys Trp Gln Asn Val Hie Phe His Cys Ser

485 490 495

Gly Ala Pro Val Ala Pro Leu Gln

500

<210> 19 <211> 433 <212> PRT <213> Homo sapiens

<220>
<221> misc feature

c223> Incyte Clone Number: 1512656

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275
                                    28D
Ile Leu Leu Ser Glu Pro Glu Asn Ala Asp Ser Leu Met Leu
Val Amp Phe Glu Tyr Ser Ser Tyr Amn Tyr Arg Gly Phe Amp Ile
Oly Ash His Phe Cys Glu Trp Val Tyr Asp Tyr Thr His Glu Glu
Trp Pro Phe Tyr Lys Ala Arg Pro The Asp Tyr Pro Thr Glm Glu
                335
                                     340
                                                         345
Oln Oln Leu His Phe Ile Arg His Tyr Leu Ala Elu Ala Lys Lys
                350
                                    355
Gly Glu Thr Leu Ser Glu Glu Glu Glu Arg Lyz Leu Glu Glu Asp
                365
                                    370
Lou Leu Val Glu Val Ser Arg Tyr Ala Lou Ala Ser His Phe Pho
                380
                                    385
Trp Gly Leu Trp Ser Ile Leu Gln Ala Ser Met Ser Thr Ile Glu
                395
                                    400
Phe Gly Tyr Leu Asp Tyr Ala Gln Ser Arg Phe Gln Phe Tyr Phe
                410
                                    415
                                                         420
Gln Gin Lys Gly Gln Leu Thr Ser Val His Ser Sor Sor
                425
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<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone Number: 2098635

<400> 20

BNSDODIE RWY 000672HA2TES

Met Ser Leo Cys Gly Ala Arg Ala Asa Ala Lys Met Met Ala Ala Tyr Asn Gly Gly Thr Ser Ala Ala Ala Ala Gly Kie Kie Hie Hie His His Eis His Leu Pro His Leu Pro Pro Pro His Leu Leu His His His His Pro Gln His His Leu His Pro Gly Ser Ala Ala Ala 50 55 Val His Pro Val Oln Gln His Thr Sur Ser Ala Ala Ala Ala Ala 65 70 Ala Ala Ala Ala Ala Ala Ala Met Leu Asn Pro Gly Gln Gln ₽\$ Gim Pro Tyr Phe Pro Ser Pro Ala Pro Gly Gin Ala Pro Gly Pro 100 95 Ala Ala Ala Ala Pro Ala Glo Val Glo Ala Ala Ala Ala Ala Thr LIO 115 Val Lys Ala Ris His His Gln His Ser His His Pro Gln Gln Gln 125 130 Leu Asp The Glu Pro Asp Arg Pro The Gly Tyr Gly Ala Phe Gly 140 145 Val Val Trp Ser Val Thr Asp Pro Arg Asp Gly Lys Arg Val Ala 355 160 Leu Lys Lys Met Pro Asn Val Phe Gln Asn Leu Val Ser Cys Lys

				170					175					180
71	₹7 4 7	Dine	2		Lau	Lect	Met	Leu		lihe	Pho	avi1	Нав	
₩ .A	• 44	J. 154'4	V-3	185	20.4				150			,		195
neA	val	Leu	Ser		Leu	Авр	Ile	Leu	Gln	PYC	PTC	His	ıle	Азр
				200					205					210
TYX	Phe	Glu	Glu	Il≑	Tyr	ľeV	Val	יומד	@lu	L≙u	Met	Gln	Ser	Yab
				215					220					225
Leu	нів	Lya	Ile	Ile	Val	∄⇔.r	Pro	Glo		Leu	Ser	Eer	Aep	Kis
				330			_		235		_	_	_	240
Val	Lyd	Va1	Ph∈		Tyr	Gln	Ile	Leu		OTA	Γ÷й	Lye	Tyr	
		_		245	_				250	T		e/1	×	255 5-24
His	Ser	Mla	Gly		Leu	HIB	Arg	vah		гуя	FIG	GLY	жви	270
_	v. 3			250	Cy e	1143	T	T	265	rSee) nn	Dh#	സം	
Lau	Val	Agn	ROL	275	∨ув	VAI	₩	нýю	280	C.3.19	n.sy	E 44/5	V# 1	205
n l s	2	325 T	Glu		Leu	App	Glu.	Rar		нiя	Met	Thr	Gln	_
ыа	wrA	441	GIL	290	LUG	пор			295		•			300
Wal	Va1	Thr	Gla		Tyr	Arq	Ala	Pro	Glo	I1e	Leu	Met	Giy	9er
,				305	-	_			310					315
Arq	Hie	Tyr	Ser	Aan	Ala	Ils	Авр	Ile	Trp	Ser	val	Gly	Сув	Ile
_				320					335					330
Ph≑	Ala	glų	Ьфц	Leu	Gly	Arg	Arg	Ile	rea	Ph≘	Gln	ala	Gln	
				335					340	_		=		345
Pro	Ile	Gln	Gln		Авр	Leu	Ilo	The		Lau	Lau	GIY	LPI	PEO
		_		350		_,			355	1	. 1.	T	31-	360
Ser	Leu	Glu	Ala		Arg	тпт	AIZ	Cye	310	ату	AT 6	БУВ	ara	375
		*	. .	365	His	Tarm	@1n	Dec		Lenn	Pro	VAI	I -= 11	
IIG	Per	Arg	GIY	OSE OSE		ما وربي	QAII.	720	385					390
min w	T.211	Car	Sar			Thr	нів	Glu			нiэ	Leu	Leu	Сув
1111	TICU	961		395					40D					405
Ara	Met	Lena	Val			Pro	Şer	Lys	Arg	Ile	Вет	Ala	Lys	λsp
_				410					415					430
Ala	Leu	Ala	ніе	Pro	Тут	Leu	Asp	Glu	Gly	Arg	Leu	. Arg	Tyr	His
				425					430					435
Thr	Cys	Met	Cya	Lys	Cys	Cyt	Pb¢	Sex			Thr	Gly	Arg	Val
				440			-		445		-	-1	-	450
Tyr	Thr	Ser	. Yet			Pro	Val	. The			: гув	hue	, wel	Aep 465
				455		0.44		. 5741	460		. T/= 1	Vare	o atu	Ile
Thr	Phe	ı Olu	. Буя) ster	àcı	4.241	. #+5 475			, 41,1	. 411	490
Tio	. rada	പ	. Time	47L Σ12		Glu	. Glr	ı Glr		-	ABI	. Ars	r Va]	Pro
175			I FILE	405					490					495
f.m	(fig.	, Tl=	э Дят	1 FTG	> (31π	. Şer	Ale	Ale			ge:	Phe	: Ila	Ser
				500	3				509	5				510
Ber	Thi	va]	LAl	a Gli	ı Pro) Ger	: Glı	1 Met	Pro) Pro) ĝej	Pro	o Lea	ı Val
				519					520					525
Tr	01 1	ı												
_														

<210> 21 <211> 322

<212> PRT

<213> Homo sapiens

<220>

<321> misc_feature
<223> Incyte Clone Number: 2446646

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<210> 22

<211> 802

<212> PRT

<213> Nomo sapiena

<220>

<221> misc_feature

<223> Incyte Clone Number: 2764911

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				395					400					405
The	Aen	Val	Ala		Bor	Ala	Met	Ket	-	Asp	Ser	Pro	Ph¢	
Gln	нів	туг	Aap		Азр	Leu	Lye	Авр		Pro	Leu	Gly	Glu	
ßer	Phe	8er	Il¢	•	Axg	Lys	Сув	Væl		Lys	Lys	Ser	Agri	
Ala	Phe	Ala	Val		Ile	Ile	Ser	Lув		Met	Glu	Ala	Aan	
Gln	Lys	Glu	Ile	Thr 470	Ala	Leu	Glu	Leu	•	Glu	Oly	His	Pro	
Ile	Val	Lув	Leu	H18 495	Glu	Val	Phe	нів	Aep 490	Gln	Leu	Hie	Thr	
Leu	Val	Met	Gl u	Leu 500	Leu	Aen	Gly	ው ኒሃ	Glu 505	Ն ¢ ա	Phe	g lų	Arg	Ile 510
Lув	Lys	ьув	Lya	H18 515	Sye	Ber	Glu	Thr	Glu 520	Ala	EBT	Tyr	ĭla	Met 525
Arg	Lys	Leu	Val	9¢≭ 530	Ala	Vel	9er	Hig	Met 535	His	Asp	Val	gly	Val. 540
Val	His	Arg	Aep	Leu 545	Lye	Pro	Glu	Asn	Leu 550	Leu	₽he	Thr	Asp	Glu 555
Aen	geA	Аеп	Leu	Glu 550	Tle	Гув	Ila	Lle	Asp 565	Fhe	Gly	\$ho	Ala	Arg 570
Leu	Lyz	Pro	Pro	Авр 575	Asn	Gln	Pro	Leu	Lya 580	Thr	Pro	Сув	Phe	Thr 585
Leu	Hip	ፒን።	Ala	Ala 590	Pro	⊕ 1⊓	L∉ų	L-⊊u	Asn 595	Gln	Ann	Gly	Tyr	A#p 690
				605	_				610	Ile		_		515
				€20					625	Asp				630
Сув	Thr	Ser	Ala	Val 635	Glu	Ile	Met	Lya	Lys 640	Ile	Lув	Lув	Gly	Авр 645
				€50				•	655	Val				660
	-			665	_				670	Yab			•	675
	_			680		_	_		605	Tip			-	590
				Б95					700	Pro	_			705
		_		710				_	715	_				яіа 720
			_	725				_	730	Cya				735
				740					745					무수박 750
				755					760	Glu				765
				770			•		775	Pro		_		780
				785			Ber	Asn	neA Oer	FTC	Glu	Thr	Len	Phe 795
Gln	Phe	Sex	Asp	800 6er	Val	ala								

WO 00/06728 PCT/US99/17132

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Thr Leu Pro Pro Ala Ala Leu Glu Pro Gin Thr Thr Val Ile Hiz
                350
                                     355
Ast Pro Val Asp Gly Ile Lys Glu Ser Ser Asp Ser Ala Asn Thr
                                     370
Thr Ile Glu Asp Glu Asp Ala Lys Ala Pro Arg Val Pro Asp Ile
                                     365
Leu Ser Ser Val Arg Arg Gly Ser Gly Ala Pro Glu Ala Glu Gly
                395
                                     400
Pro Leu Pro Cys Pro Ser Pro Ala Pro Phe Gly Pro Leu Pro Ala
                410
                                     415
Pro Ber Pro Arg Ile Ser Asp Ile Leu Asn Ser Val Arg Arg Gly
                                     430
Ser Gly Thr Pro Glu Ala Glu Gly Pro Leu Ser Ala Gly Pro Pro
                440
                                     445
                                                         450
Pro Cys Leu Ser Pro Ala Lou Lou Sly Pro Leu Ser Ser Pro Ser
                 455
                                     460
Pro Arg Ile Ser Asp Ile Leu Asn Ser Val Arg Arg Gly Ser Gly
                 470
                                     475
The Pro Glu Ala Lys Gly Pro Ser Pro Val Gly Pro Pro Pro Cys
                 485
                                     490
                                                         495
Pro Ser Pro Thr Ile Pro Gly Pro Leu Pro Thr Pro Ser Arg Lys
                500
                                     505
Gin Glu Ilo Ilo bys Thr Thr Glu Cln Leo Ile Glu Ala Val Asn
                515
                                     520
Asn Gly Asp Phe Glu Ala Tyr Ala Lys Ile Cys Asp Pro Gly Leu
                530
                                     535
Thr Ser Phe Glu Pro Glu Ala Leu Gly Asn Leu Val Glu Gly Met
                                     550
Amp Pho Ris Arg Pho Tyr Phe Glu Am Leu Leu Ala Lye Am Ser
                560
                                     565
Lye Pro Ile His Thr Thr Ile Leu Asn Pro Ris Val Ris Val Ile
Gly Glu Aap Ala Ala Cys Ile Ala Tyr Ile Arg Leu Thr Gln Tyr
Ile Asp Gly Gln Gly Arg Pro Arg Thr Ber Gln Ser Glu Glu Thr
                                     610
Arg Val Trp His Arg Arg Asp Gly Lys Trp Gln Asn Val His Phe
                620
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His Cys Ser Gly Ala Pro Val Ala Pro Lou Gln
                635
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<211> 588

<212> PRT

<213> Homo sapiene

<320>

BNSE/CXXX RWC: 0006728A2TLS

<221> misc_feature

<223> Incyte Clone Number: 067967

<400> 24

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Pro Gly Ala Gly Leu Pro Pro Gln Gln Arg Arg Leu Gly Amp Gly

20 25 30
Val Tyr Asp Thr Phe Net Met Ile Asp Glu Thr Lys Cys Pro Pro

				35					40					45
Cya	Ber	Aan	Val		Çya	Asti	Pro	Ser		Pro	PTO	∂र-∓	Bro (rg
				50					55					60
Атд	Гөл	Aan	Met	Thr 55	Thr	Glu	СП	Phe	70	GIA	Авр	тн	Thr	75
нів	Phe	Leu	Дар		Gly	Glu	Net	Lys		Glu	Gln	Гел	Phe (Sln
				90					95					90
Glu	Pho	Gly	Asn	Arg 95	Lyp	9≑≭	Acn	The	100	ĠΤŪ	3CX	Wab	Q1y	105 105
Ser	ABD	ser	Glu		Суз	Ser	PID	Thr		Ser	Gln	Gly	Lys .	6er
				110					115					120
Эer	увъ	Cys	Leu	Aan 125	Thr	Val	Lya	Ber	13¢	eer	HEI	Ser	Lys .	135
Pro	Lvs	Val	Val		Leu	Thr	Pro	Glu		Ala	L⊭d	Lye	Glī	Tyr
				140					143					150
ГАВ	Hie	Ria	Leu	Thr 155	Ala	Tyr	Glu	TAB	160	GTO	ITe	119	Asn	19I 165
Pro	Glu	Il∈	Tvr	Phe	Val	Gly	Pro	Asn		Lys	Lys	Arg	His	
				170					175					160
Val	IJe	Gly	Gly		Aan	Apn	gly	Gly	Tyr 190	qeA	Ъзр	АТа	Asp	GLY 195
Ala	Tyr	Ile	нів	105 Vel	Pro	Arg	Авр	Hie		Ala	Tyr	Arg	Tyr	
				200					205					210
Val	Lou	ГЛЭ	Ile		Gly	Lya	GLY	Ber	220	91y	GTU	Val	Ala	225
Val	Tyr	Asc	нів	215 Lys	Leu	Arg	Gln	Tyr		Ala	Leu	Lye	Met	
				230					235					24D
Arg	Asn	Glu	Lyp	Arg 245	Ph¢	His	Arg	Gln	Ala 250	Ale	Blu	BLU	Il¢	भरप 255
T.l.e.	Leu	Glu	a Hie		Lya	Lys	Gln	Авр		Thr	Gly	Ber	Mat	
				260					265					270
Val	Ile	Hie	: Met		alu	Ser	Phe	Thr	Phe 230		Agn	RIE	Val	285
Met	Ala	Phe	• Glu	275 Leu	Leu	Ser	Ile	Авр			Glu	Leu	Ile	
				290					295					300
Lys	ARI	Lye	Phe			Phe	9¢r	Val	310 310		. A\$T	Arg	Lys	315
Ala	Gli	ı Ben	r Ile	305 Leu		ser	Leu	Aep			ніа	Lya	Aan	
				330					325	•				330
I1e	: Ile	Ł Hi,	≉ Суя			Ly#	Pro) Glu	1 ሕመር 340	i Il¢	: L¢u	i p¢4	ĿŸ#	д1 в 345
Hie	. Gly	Ar	g 5e:	335 Ser	The	Lye	val	lle			Gly	z Ser	ser	Сув
				350					353	5				360
Phe	2 91 1	ı Ty:	r Gli	1 Lye 365		ı Tyr	Thi	Tyr	: Ile 370		7 Aex	Mrg	Phe	375
Arc	a Ala	ı Pr	o Gli			. Leu	. Gly	/ Bez	_		Ser	Tha	BEO	
				380	>				355	5				390
ABJ	, Il	e Tr	p ₽¢:	r Phe 39!		y Cye	ı Ile	e re	ነ ል ጊል 401	3 G11 N	ı L≙t	ı Let	Thr	405
(1) r	n Pri	o Le	u Ph			y Gli	ı Ası	o Gli		-	Gli	ı Lası	ı Ala	
				411)				41	5				420
Met	t Ne	F G1	u Le			y Nel	- Pro	o Per	P۲۰ 43		a Lei	u Lel	ı Əlu	435 354
He	r Lv	э Ах	g Al	42! a Ly:		r Ph	a Il	a Aei			e (31)	y Il	e Pro	
				44	D .				44	5				450
$\mathbf{T}_{\mathbf{y}}$	r Çy	# 9¢	r Va	1 Th	t Th	r Gl	n Al	3 AB	b ay	y Ar	g Va	I VB.	l Leu	ı Vall

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455
                                     460
Giy Gly Arg Ser Arg Arg Gly Lys Lys Arg Gly Pro Pro Gly Ser
                470
Lys Asp Trp Gly Thr Ala Leo Lys Gly Cys Asp Asp Tyr Leu Phe
The Glu Phe Leu Lys Arg Cys Leu His Trp Asp Pro Sor Ala Arg
                500
                                     505
Leu Thr Pro Ala Gln Ala Leu Arg His Pro Trp Ile Ser Lys Ser
                515
                                     520
Val Pro Arg Pro Leu Thr Thr Ile Asp Lys Val Ser Gly Lys Arg
                530
                                     535
Val Val Asn Pro Ala Ser Ala Phe Gin Gly Leu Gly Ser Lys Leu
                545
                                     550
Pro Pro Val Val Gly Ile Ala Asn Lys Lou Lys Ala Asn Lou Met
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Ber Glu Thr Asn Gly Ser Ile Pro Leu Cys Ser Val Leu Pro Lys
                575
                                     500
Leu Ile Ser
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<211> 389

<212> PRT

<213> Homo sapiene

₹220>

<221> misc feature

<223> Incyte Clone Number: 346275

<400> 25

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Ber Asp Phe Gly Leu Ser Lys Met Glu Gly Lys Gly Asp Val Met
                                    205
Ser Thr Ala Cys Gly Thr Pro Gly Tyr Val Ala Pro Glu Val Lou
                                    220
                215
Ala Gln Lye Pro Tyr Ser Lys Ala Val Aep Cys Trp Ser Ile Gly
                                    235
                230
Val Ile Ala Tyr Ile Leu Leu Cys Gly Tyr Pro Pro Phe Tyr Asp
                                     250
                245
Glu Asn Asp Ser Lys Lou Phe Glu Gln Ile Lou Lys Ala Glu Tyr
                                     265
                260
Glu Phe Amp Ser Pro Tyr Trp Amp Amp Ile Ser Amp Ser Ala Lym
                                                         285
                275
Amp Phe lle Arg Amn Lou Met Glu Lym Amp Pro Amn Lym Arg Tyr
                                     295
                230
Thr Cys Glu Gln Ala Ala Arg His Pro Trp Ile Ala Gly Asp Thr
                                    320
Ala Leu Asn Lys Asn Ile Sis Glu Ser Val Ser Ala Gln Ile Arg
                                    325
                330
Lys Asn the Ala Lys Ser Lys Trp Arg Gln Ala Phe Asn Ala Thr
                                    340
                335
Ala Val Val Arg His Met Arg Lys Leu His Leu Gly Ber Ber Leu
                                     355
                350
Asp Ser Ser Asn Ala Ser Val Ser Ser Ser Leu Ser Leu Ala Ser
                                     270
                365
Gln Lya Amp Cya Ala Tyr Val Ala Lym Pro Glu Ber Leu Ber
                                     385
                380
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<210> 26
<211> 343
<212> PRT
<213> Horo sepiens
<220>
<221> misc feature

<223> Incyte Clone Number: 283746

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Cys Ser Phe Leu Asp Asp Leu Leu Glu Leu Arg Asp Glu Glu Leu
                140
                                     145
ser Lys Glu Ser Gln Glu Thr Asn Trp Phe Ser Als Pro Ser Als
                                     160
Leu Arg Val Tyr Gly Gln Tyr Leu Aen Leu Asp Lys Asp His Asn
                170
                                     175
Gly Met Leu Ser Lys Glu Glu Leu Ser Arg Tyr Gly Thr Ala Thr
                185
                                     190
Met Thr Asn Val Phe Leu Asp Arg Val Phe Gln Glu Cys Leu Thr
                200
                                     205
Tyr Asp Gly Glu Not Asp Tyr Lys Thr Tyr Leu Asp Phe Val Leu
                215
                                     220
Ala Leu Glu Asn Arg Lys Glu Pro Ala Ala Leu Gln Tyr Ile Pho
                230
                                     235
Lys Leu Leu Asp Ile Glu Asn Lys Gly Tyr Leu Asn Val Phe Ser
                                     250
                245
Leu Asn Tyr Phe Phe Arg Ala Ile Gln Glu Leu Met Lys Ile His
                260
                                     265
                                                         270
Gly Gln Amp Pro Val Ber Phe Gln Amp Val Lys Amp Glu Ile Phe
                275
                                     280
Asp Met Val Lye Pro Lys Asp Pro Leu Lys Ile Ser Leu Gln Asp
                290
                                     295
how The Asn Ser Asn Gln Gly App Thr Val Thr Thr Ile Lew The
                                     310
Asp Leu Asn Gly Phe Trp Thr Tyr Glu Asn Arg Glo Ala Leu Val
                                     325
Ala Asn Asp Ser Clu Asn Ser Ala Asp Leu Asp Asp Thr
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<210> 27 <211> 184

<213> Homo sapiens

<220>

<221> misc feature

<223> Incyte Clone Number: 2696537

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<212> PRT

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 His Trp Lau Ser Asn Lau Clu Ser Thr His Trp Lau Glu His Tle
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 Ser Gly Lys Thr Ser Val Val Val His Cyr Ser App Gly Trp Asp
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 Arg Thr Ala Gin Leu Thr Ser Lou Ala Mot Leu Mot Leu Asp Oly
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 Tyr Tyr Arg Thx ile Arg Cly Phe Glu Val Leu Val Glu Lys Glu
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 Trp Leu Ser Phe Gly His Arg Phe Glo Leu Arg Val Gly His Gly
                 סלו
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 Asp Lys Asn Kis Ala Asp Ala Asp Arg Ser Pro Val Phe Leu Gln
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Pha Ile Asp Cya Val Trp Gln Met Thr Arg Gln Phe Pro Thr Ala
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Phe Glu Phe Asn Glu Tyr Phe Leu Ile Thr Ile Leu Asp Ric Leu
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Tyr Ser Cys Leu Pha Gly Thr the Leu Cys Aen Ser Glu Gln Gin
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Arg Gly Lys Glu Asn Lew Pro Lys Arg Thr Val Ser Lou Trp Sor
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Tyr lle Agn Ser Gln Leu Glu Asp Phe Thr Agn Pro Leu Tyr Gly
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Ser Tyr Ser Asn His Val Leu Tyr Pro Val Ala Ser Met Arg His
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Gly.	Asp	Læu	Leu		Thr	Gly	qeA	Lye	G1y SS	Ģly	Arg	Val	Val	11e 60
Phe	@1n	Arg	Glu	91 n 65	3 lu	Asn	Lys	8er	A219 70	PTO	нів	Ber	Arg	Gly 75
Glu	Tyr	ABD	Val	Tyr 80	Ber	Thr	Phe	aln	Ser 95	нів	Glu	Pro	Glu	Phe 90
Asp	_			95					100					105
Arg	Trp	Lau	Pro	Ğln 110	Gln	ABII	Ala	Ala	H16 115	Ph∈	Leu	Leu	Ser	Thr 120
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_				Tyr 140					145					150
_				Ila 155					150					165
	_			Val 170					175					190
			-	His 185					190					195
				200 200					205					210
				Άթ ը 315					220					225
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				Cys 245					250					255
				Cye 250					265					270
				Phe 275					200					285
				11a 290					395					300
				Tyr 305					310					315
	_	_		Aen 320					325					320
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_				350					355					Авр 360
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				380					385	ı				Glu 390
				395					400	l				The 405
			•	410					415	i				130 130
				425					430	ı				ABD 435
Val	Ile	. Als	. Val	. Ale	Ala	Thr	Aen:	Aer	Let	гуг	· Ile	≥ Phe	e Glr	Аар

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WO 00/06728

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(63) Related by Continuation (CON) or Continuation-in-Part (CIP) to Earlier Applications

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(57) Abstract

The invention provides human phosphorylation effectors (PHSP) and polynucleotides which identify and encode PHSP. The invention also provides expression vectors, host cells, antibodies, agonists, and antagonists. The invention also provides methods for diagnosing, treating, or preventing disorders associated with expression of PHSP.

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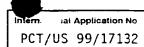
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo ni,

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	To.
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	WO 98 11234 A (HAWKINS PHILLIP R ;INCYTE PHARMA INC (US); AU YOUNG JANICE (US); G) 19 March 1998 (1998-03-19) the whole document WO 97 02347 A (INCYTE PHARMA INC) 23 January 1997 (1997-01-23) the whole document WALDEN, P.D. AND COWAN, N.J.: "a novel 205-kilodalton testis-specific serine/threonine protein kinase associated with microtubules of the spermatid manchette" MOLECULAR AND CELLULAR BIOLOGY, vol. 13, 1993, pages 7625-7635, XP002121150 the whole document NAGASE, T., ET AL.: "prediction of the coding sequences of unidentified human genes. IX. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro" DNA RESEARCH, vol. 5, 1998, pages 31-39, XP002121152 especially Table 2 + 3 the whole document HILLIER, L., ET AL.: "the WashU-Merck EST project" EMBL SEQUENCE DATA LIBRARY, 25 March 1995 (1995-03-25), XP002121151 heidelberg, germany accession no. t77135 WO 97 48802 A (HAWKINS PHILLIP R ;INCYTE PHARMA INC (US); AU YOUNG JANICE (US); H) 24 December 1997 (1997-12-24) the whole document WO 99 04265 A (SAHIN UGUR ;TURECI OZLEM (DE); PFREUNDSCHUH MICHAEL (DE); GOUT IVA) 28 January 1999 (1999-01-28) pages 1-7,537,578,709 claims

Inte. .ational application No

INTERNATIONAL SEARCH REPORT

PCT/US 99/17132

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)
This international Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons
Claims Nos. because they relate to subject matter not required to be searched by this Authomy, namely Remark: Although claim 19 is directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.
2. X Claims Nos 17, 18, 20 because they relate to parts of the international Application that do not comply with the prescribed requirements to such an extent that no meaningful international Search can be carried out, specifically see FURTHER INFORMATION sheet PCT/ISA/210
3. Claims Nos because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).
Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)
This international Searching Authority found multiple inventions in this international application, as follows. See additional sheets
As all required additional search fees were timely paid by the applicant, this international Search Report covers all searchable claims.
2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos
No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims. Nos 1-20 partially
Remark on Protest The additional search fees were accompanied by the applicant's protest. No protest accompanied the payment of additional search fees.

Form PCT/ISA/210 (continuation of first sneet (1)) (July 1998)

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

1. Claims: 1-20 partially

Polynucleotide and polypeptide sequences that show homology to Protein Kinases; especially SEQIDs 1,12 and 32,43; the recombinant expression of the same and uses thereof.

2. Claims: 1-20 partially

Polynucleotide and polypeptide sequences that show homology to PKC-potentiated inhibitory protein of PP1; especially SEQIDs 2 and 33; the recombinant expression of the same and uses thereof.

3. Claims: 1-20 partially

Polynucleotide and polypeptide sequences that show homology to STE20-like Protein Kinases; especially SEQIDs 3 and 34; the recombinant expression of the same and uses thereof.

4. Claims: 1-20 partially

Polynucleotide and polypeptide sequences that show homology to Phosphofructokinases; especially SEQIDs 4 and 35; the recombinant expression of the same and uses thereof.

5. Claims: 1-20 partially

Polynucleotide and polypeptide sequences that show homology to Serin/Threonine Protein Kinases; especially SEQIDs 5,6,10 and 36.37,41; the recombinant expression of the same and uses thereof.

6. Claims: 1-20 partially

Polynucleotide and polypeptide sequences that show homology to Phosphatidylinositol-3-kinases; especially SEQIDs 7 and 38; the recombinant expression of the same and uses thereof.

7. Claims: 1-20 partially

Polynucleotide and polypeptide sequences that show homology to Tyrosine or Tyrosine/serine Protein Kinases; especially SEQIDs 8,13,21 and 39,44,52; the recombinant expression of the same and uses thereof.

8. Claims: 1-20 partially

Polynucleotide and polypeptide sequences that show homology

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

to Calcium /Calmodulin dependent Protein Kinases; especially SEQIDs 9.18,23.25 and 40,49,54,56; the recombinant expression of the same and uses thereof.

9. Claims: 1-20 partially

Polynucleotide and polypeptide sequences that show homology to Tyrosine Phosphatases or Dual specificity phosphatases; especially SEQIDs 11,29,30 and 42,60,61; the recombinant expression of the same and uses thereof.

10. Claims: 1-20 partially

Polynucleotide and polypeptide sequences that show homology to PEST phosphatase interacting protein; especially SEQIDs 14 and 45; the recombinant expression of the same and uses thereof.

11. Claims: 1-20 partially

Polynucleotide and polypeptide sequences that show homology to SH3-binding proteins; especially SEQIDs 15 and 46; the recombinant expression of the same and uses thereof.

12. Claims: 1-20 partially

Polynucleotide and polypeptide sequences that show homology to NIK-kinases; especially SEQIDs 16 and 47; the recombinant expression of the same and uses thereof.

13. Claims: 1-20 partially

Polynucleotide and polypeptide sequences that show homology to Inferferon-induced PK regulators; especially SEQIDs 17 and 48; the recombinant expression of the same and uses thereof.

14. Claims: 1-20 partially

Polynucleotide and polypeptide sequences that show homology to Choline-kinases; especially SEQIDs 19 and 50; the recombinant expression of the same and uses thereof.

15. Claims: 1-20 partially

Polynucleotide and polypeptide sequences that show homology to MAP-related Protein kinases; especially SEQIDs 20 and 51; the recombinant expression of the same and uses thereof.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

16. Claims: 1-20 partially

Polynucleotide and polypeptide sequences that show homology to Ribosomal S6 Protein kinases; especially SEQIDs 22 and 53; the recombinant expression of the same and uses thereof.

17. Claims: 1-20 partially

Polynucleotide and polypeptide sequences that show homology to Protein kinases Dyrk2; especially SEQIDs 24 and 55; the recombinant expression of the same and uses thereof.

18. Claims: 1-20 partially

Polynucleotide and polypeptide sequences that show homology to Protein Phosphatases 2A; especially SEQIDs 26,28,31 and 57,59,62; the recombinant expression of the same and uses thereof.

19. Claims: 1-20 partially

Polynucleotide and polypeptide sequences that show homology to MAP-kinase Phosphatases; especially SEQIDs 27 and 58; the recombinant expression of the same and uses thereof.

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FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.2

Glaims Nos.: 17,18,20

Claims 17,18 and in part 20 refer to an antagonist and agonist of the polypeptides without giving a true technical characterization. Moreover, no such compounds are defined in the application. In consequence, the scope of said claims is ambiguous and vague, and their subject-matter is not sufficiently disclosed and supported (Art. 5 and 6 PCT). No search can be carried out for such purely speculative claims whose wording is, in fact, a mere recitation of the reults to be achieved.

The applicant's attention is drawn to the fact that claims, or parts of claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

- Julier

PCT/US 99/17132

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